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Figure 1. Oligonucleotide Primers for QuikChange Mutagenesis

V93E#1

5'-gAACATCCCCAAGATgAACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 6)

V93E#2

5'-CTTTTCTCTAATAgTgggTTCATCTTggggATgTTC-3' (SEQ ID NO: 7)

V93R#1

5'-gAACATCCCCAAGATAgACCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 8)

V93R#2

5'-CTTTTCTCTAATAgTgggTCTATCTTggggATgTTC-3' (SEQ ID NO: 9)

V93N#1

5'-gAACATCCCCAAGATAACCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 10)

V93N#2

5'-CTTTTCTCTAATAgTggggTTATCTTggggATgTTC-3' (SEQ ID NO: 11)

V93H#1

5'-gAACATCCCCAAGATCACCCCACTATTAgAgAAAAAg-3' (SEQ ID NO: 12)

V93H#2

5'-CTTTTCTCTAATAgTggggTgATCTTggggATgTTC-3' (SEQ ID NO: 13)

V93X (for saturation mutagenesis; obtained V93G and V93L mutants from library)

5'-(Phosphate)gAACATCCCCAAGATNNKCCCACTATTAgAgAAAAAg-3'
(SEQ ID NO: 14)

V93K#1

5'-gAACATCCCCAAGATAAACCCACTATTAgAg-3' (SEQ ID NO: 43)

V93K#2

5'-CTCTAATAgTgggTTTATCTTggggATgTTC-3' (SEQ ID NO: 44)

QCM#1 5'-(Phosphate)gAACATCCCCAAGATgCACCCACTATTAgAgAAAAAg-
(SEQ ID NO: 45)'
Alanine

QCM#2 5'-(Phosphate)gAACATCCCCAAGATgACCCCACTATTAgAgAAAAAg-3'
(SEQ ID NO: 46)
Aspartic Acid

QCM#3 5'-(Phosphate)gAACATCCCCAAGATTgCCCCCACTATTAgAgAAAAAg-3'
(SEQ ID NO: 47)
Cysteine

QCM#4 5'-
(Phosphate)gAACATCCCCAAGATATACCCCACTATTAgAgAAAAAg-3'
(SEQ ID NO: 48)
Isoleucine

QCM#5 5'-(Phosphate)gAACATCCCCAAGATATgCCCCTACTATTAgAgAAAAAg-3'
(SEQ ID NO: 49)
Methionine

QCM#6 5'-(Phosphate)gAACATCCCCAAGATTTCCCCCACTATTAgAgAAAAAg-3'
(SEQ ID NO: 50)
Phenylalanine

QCM#7 5'-(Phosphate)gAACATCCCCAAGATCCTCCCCTACTATTAgAgAAAAAg-3'
(SEQ ID NO: 51)
Proline

QCM#8 5'-(Phosphate)gAACATCCCCAAGATAgCCCCCACTATTAgAgAAAAAg-3'
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Serine

QCM#9 5'-(Phosphate)gAACATCCCCAAGATACACCCCACTATTAgAgAAAAAg-3'
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Threonine

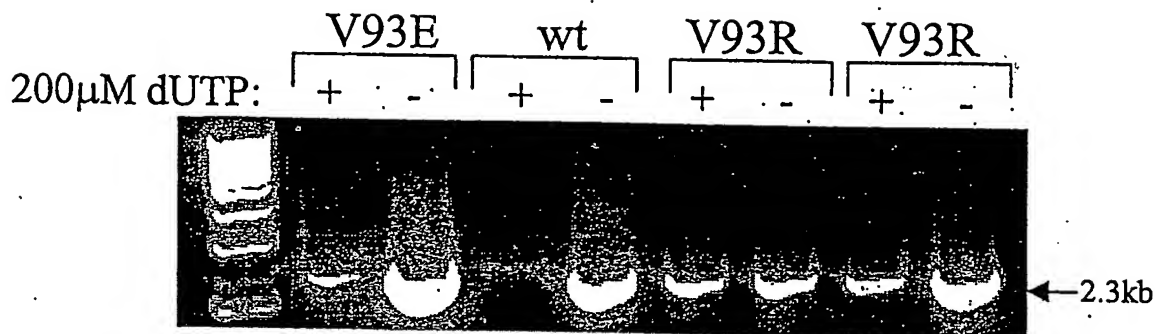
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(SEQ ID NO: 54)

Tyrosine

QCM#11 5'-(Phosphate)gAACATCCCCAAGATTggCCCACTATTAgAgAAAAAg-3'
(SEQ ID NO: 55)

Tryptophan

a.)



b.)

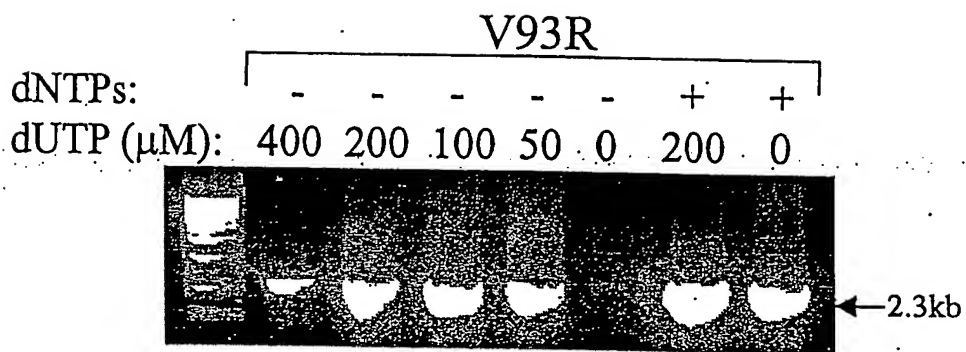


Figure 2

Figure 3: Protein concentration, unit concentration, and specific activity of the purified Pfu V93R and V93E mutants.

<i>Pfu</i> mutant	Protein concentration	PCR Unit concentration	Specific activity (U/mg)
<i>Pfu</i>	0.0258 µg/µl	2.5U/µl	9.7×10^4
<i>Pfu</i> V93R	45 µg/µl	<u>6250U/µl</u>	<u>1.4×10^5</u>
<i>Pfu</i> V93E	35 µg/µl	<u>6250U/µl</u>	<u>1.8×10^5</u>

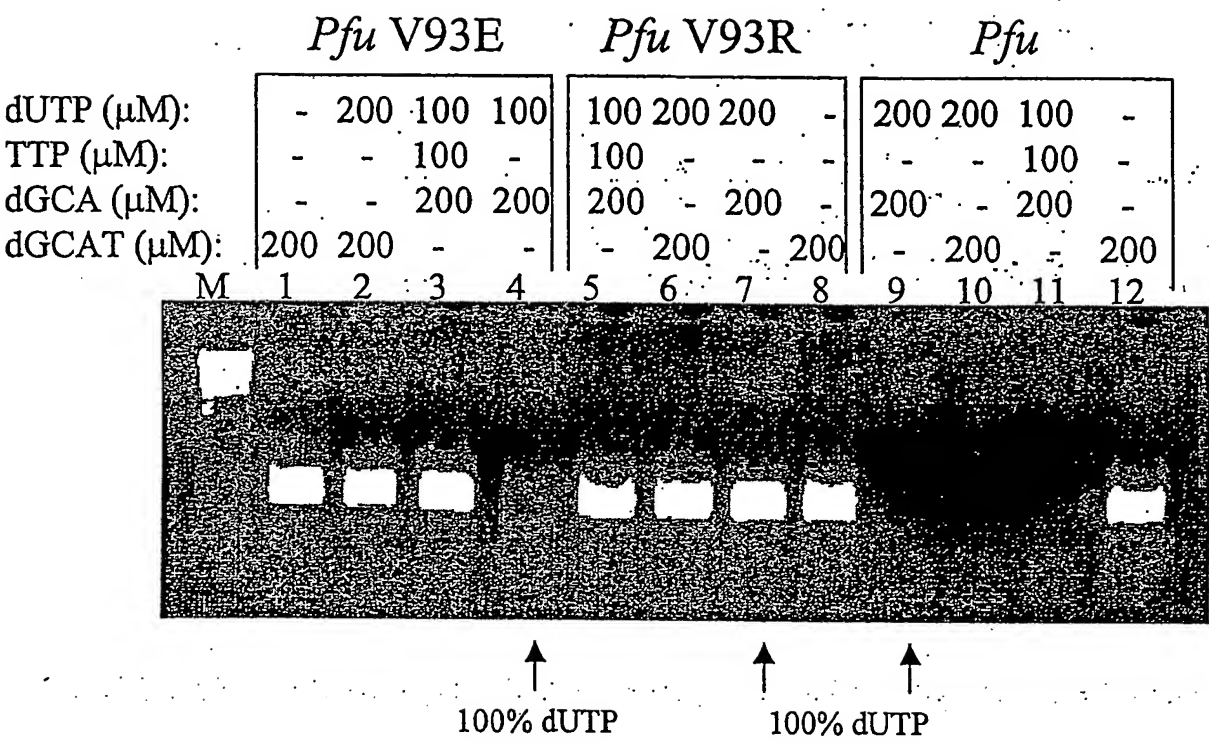


Figure 4

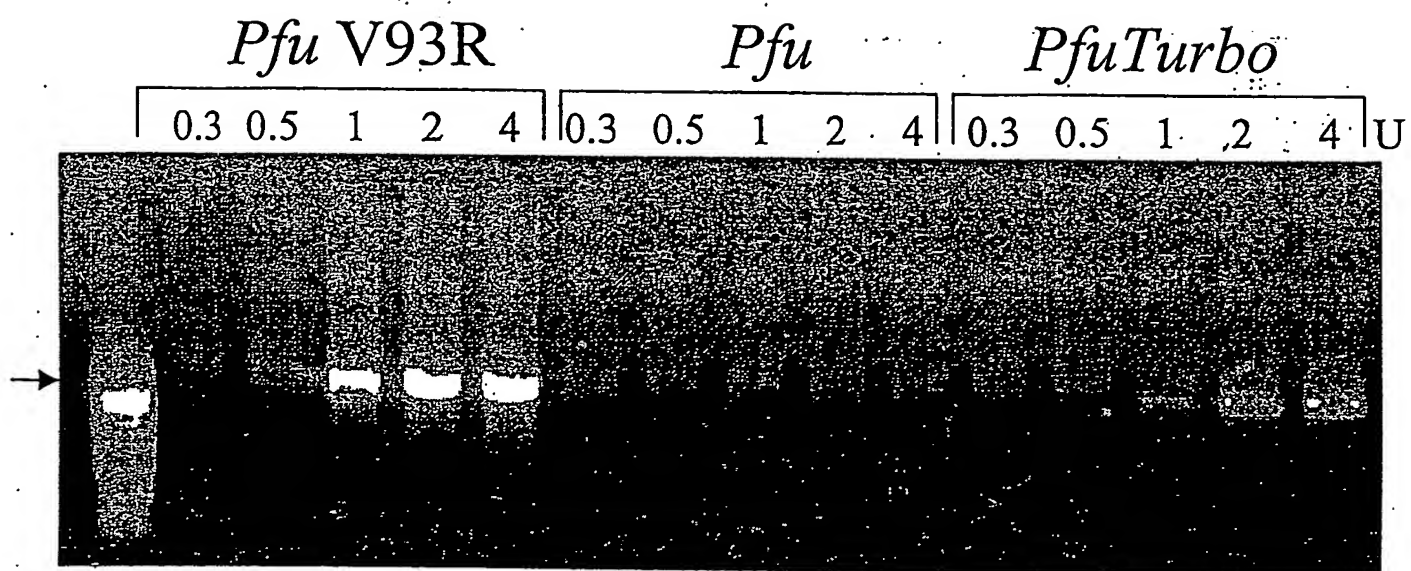


Figure 5

FIGURE 6A

PFU DNA POLYMERASE (SEQ ID NO: 17)

V93R MUTANT: GTT CAN BE MODIFIED TO BE = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: GTT CAN BE MODIFIED TO BE = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

V93D MUTANT: GTT CAN BE MODIFIED TO BE = GAT, GAC (ALL CODONS FOR ASPARTIC ACID)

V93K MUTANT: GTT CAN BE MODIFIED TO BE = AAA, AAG (ALL CODONS FOR LYSINE)

V93N MUTANT: GTT CAN BE MODIFIED TO BE = AAC, AAU (ALL CODONS FOR ASPARAGINE)

```

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACCT TTAGACCATA CATTTACGCT 120
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ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATGTTC CCACTATTAG AGAAAAAGTT 300
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KOD DNA POLYMERASE (SEQ ID NO: 18)

V93R MUTANT: GTC CAN BE MODIFIED TO BE = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: GTC CAN BE MODIFIED TO BE = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

V93D MUTANT: GTC CAN BE MODIFIED TO BE = GAT, GAC (ALL CODONS FOR ASPARTIC ACID)

V93K MUTANT: GTC CAN BE MODIFIED TO BE = AAA, AAG (ALL CODONS FOR LYSINE)

V93Q MUTANT: GTC CAN BE MODIFIED TO BE = CAA, CAG (ALL CODONS FOR GLUTAMINE)

V93N MUTANT: GTC CAN BE MODIFIED TO BE = AAC, AAU (ALL CODONS FOR ASPARAGINE)

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Vent DNA POLYMERASE (SEQ ID NO: 19)

V93R MUTANT: GTT CAN BE MODIFIED TO BE = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: GTT CAN BE MODIFIED TO BE = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

V93D MUTANT: GTT CAN BE MODIFIED TO BE = GAT, GAC (ALL CODONS FOR ASPARTIC ACID)

V93K MUTANT: GTT CAN BE MODIFIED TO BE = AAA, AAG (ALL CODONS FOR LYSINE)

V93Q MUTANT: GTT CAN BE MODIFIED TO BE = CAA, CAG (ALL CODONS FOR GLUTAMINE)

V93N MUTANT: GTT CAN BE MODIFIED TO BE = AAC, AAU (ALL CODONS FOR ASPARAGINE)

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```

Deep Vent (SEQ ID NO: 20)

V93R MUTANT: GTT CAN BE MODIFIED TO BE = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: GTT CAN BE MODIFIED TO BE = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
V93D MUTANT: GTT CAN BE MODIFIED TO BE = GAT, GAC (ALL CODONS FOR ASPARTIC ACID)
V93K MUTANT: GTT CAN BE MODIFIED TO BE = AAA, AAG (ALL CODONS FOR LYSINE)
V93Q MUTANT: GTT CAN BE MODIFIED TO BE = CAA, CAG (ALL CODONS FOR GLUTAMINE)
V93N MUTANT: GTT CAN BE MODIFIED TO BE = AAC, AAU (ALL CODONS FOR ASPARAGINE)

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ACTAAACAGA	CAGGTCTTAC	GGCATGGCTT	AACATCAAGA	AGAAGTAA		2328

V93R MUTANT: GTT CAN BE MODIFIED TO BE = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: GTT CAN BE MODIFIED TO BE = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
V93D MUTANT: GTT CAN BE MODIFIED TO BE = GAT, GAC (ALL CODONS FOR ASPARTIC ACID)
V93K MUTANT: GTT CAN BE MODIFIED TO BE = AAA, AAG (ALL CODONS FOR LYSINE)
V93Q MUTANT: GTT CAN BE MODIFIED TO BE = CAA, CAG (ALL CODONS FOR GLUTAMINE)
V93N MUTANT: GTT CAN BE MODIFIED TO BE = AAC, AAU (ALL CODONS FOR ASPARAGINE)

ATGATCCTTGACGTTGATTACATCACCGAGAATGGAAAGCCCGTCATCAGGGTCTTCAAGAAGGAGAACGGCGAGTT
CAGGATTGAATACGACCCGAGTTTCGAGCCCTACTTCTACGCGCTCCTCAGGGACGACTCTGCCATCGAAGAAATCA
AAAAGATAACCGCGGAGAGGCACGGCAGGGTCGTTAAGGTTAAGCGCGCGGAGAAGGTGAAGAAAAAGTTCTCGGC
AGGTCTGTGGAGGTCTGGGTCTCTACTTCACGCACCCGCGAGGACGTTCCGGCAATCCGCGACAAAATAAGGAAGCA
CCCCGCGGTTCATCGACATCTACGAGTACGACATACCCCTTCGCCAAGCGCTACCTCATAGACAAGGGCCTAATCCCGA
TGGAAGGTGAGGAAGAGCTTAAACTCATGTCTCTCGACATCGAGACGCTCTACCACGAGGGAGAAGAGTTTGAACC
GGGCCGATTCTGATGATAAGCTACGCCGATGAAAGCGAGGCGCGCTGATAACCTGGAAGAAGATCGACCTTCCTTA
CGTTGAGGTTGTCTCCACCGAGAAGGAGATGATTAAGCGCTTCTTGAGGGTCGTTAAGGAGAAGGACCCGACGTGC
TGATAACATAACAACGGCGACAACCTTCGACTTCGCCTACCTGAAAAAGCGCTGTGAGAAGCTTGCGGTGAGCTTTACC
CTCGGGAGGGACGGGAGCGAGCCGAAGATACAGCGCATGGGGGACAGGTTTGCGGTCGAGGTGAAGGGCAGGGTACA
CTTCGACCTTTATCCAGTCATAAGGCGCACCATAAACCTCCCGACCTACACCCTTGAGGCTGTATACGAGGCGGTTT
TCGGCAAGCCCAAGGAGAAGGTCTACGCCGAGGAGATAGCCACCGCTGGGAGACCGGCGAGGGGCTTGAGAGGGTC
GCGCGCTACTCGATGGAGGACGCGAGGGTTACCTACGAGCTTGGCAGGGAGTTCTTCCCGATGGAGGCCAGCTTTC
CAGGCTCATCGGCCAAGGCCTCTGGGACGTTTCCCCGCTCCAGCACCGGCAACCTCGTCGAGTGGTTCTCTTAAGGA
AGGCCTACGAGAGGAACGAACCTCGCTCCCAACAAGCCCGACGAGAGGGAGCTGGCGAGGAGAAGGGGGGGCTACgCC
GGTGGCTACGTCAAGGAGCCGGAGCGGGGACTGTGGGACAATATCGTGTATCTAGACTTTCGTAGTCTCTACCTTTC
AATCATAATCACCCACAACGTCTCGCCAGATACGCTCAACCGCGAGGGGTGTAGGAGCTACGACGTTGCCCGGAGG
TCGGTCACAAGTTCTGCAAGGACTTCCCCGGCTTCATTCCGAGCCTGCTCGGAAACCTGCTGGAGGAAAGGCAGAAG
ATAAGAGGAAGATGAAGGCAACTCTCGACCCGCTGGAGAAGAATCTCCTCGATTACAGGCAACGCGCTCAAGAT
TCTCGCCAACAGCTACTACGGCTACTACGGCTATGCCAGGGCAAGATGGTACTGCAGGGAGTGCGCCGAGAGCGTTA
CGGCATGGGGAAGGGAGTACATCGAAATGGTCATCAGAGAGCTTGAGGAAAAGTTTCGGTTTTAAAGTCTCTATGCA
GACACAGACGGTCTCCATGCCACCATTCTTGAGCGGACGCTGAAACAGTCAAGAAAAAGGCAATGGAGTTCTTAAA
CTATATCAATCCCAAACCTGCCCGGCTTCTCGAACTCGAATACGAGGGCTTCTACGTCAGGGGCTTCTTCGTCACGA
AGAAAAAGTACGCGGTTCATCGACGAGGAGGGCAAGATAACCACGCGCGGGCTTGAGATAGTCAGGCGCGACTGGAGC
GAGATAGCGAAGGAGACGCAGGCGAGGGTTTTGGAGGCGATACTCAGGCACGGTGACGTTGAAGAGGCCGTCAGAAT
TGTCAGGGAAGTCACCGAAAAGCTGAGCAAGTACGAGGTTCCGCCGAGAGAAGCTGGTTATCCACGAGCAGATAACGC
GCGAGCTCAAGGACTACAAGGCCACCGGCCGACGCTAGCCATAGCGAAgCGTTTGGCCCGCAGAGGTGTAAAATC
CGCCCCGGAACGTGTGATAAGCTACATCGTTCTGAAGGGCTCCGGAAGGATAGGCGACAGGGCGATTCCCTTCGACGA
GTTTCGACCCGACGAAGCACAAAGTACGATGCGGACTACTACATCGAGAACCAGGTTCTGCCGGCAGTTGAGAGAATCC
TCAGGGCCTTCGGCTACCGCAAGGAAGACCTGCGCTACCAGAAGACGAGGCAGGTCGGGCTTGGCGCGTGGCTGAAG
CCGAAGGGGAAGAAGAAGTGA

Tgo (SEQ ID NO: 22)

V93R MUTANT: GTT CAN BE MODIFIED TO BE = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
V93E MUTANT: GTT CAN BE MODIFIED TO BE = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
V93D MUTANT: GTT CAN BE MODIFIED TO BE = GAT, GAC (ALL CODONS FOR ASPARTIC ACID)
V93K MUTANT: GTT CAN BE MODIFIED TO BE = AAA, AAG (ALL CODONS FOR LYSINE)
V93Q MUTANT: GTT CAN BE MODIFIED TO BE = CAA, CAG (ALL CODONS FOR GLUTAMINE)
V93N MUTANT: GTT CAN BE MODIFIED TO BE = AAC, AAU (ALL CODONS FOR ASPARAGINE)

ATGATCCTCGATACAGACTACATAACTGAGGATGGAAAGCCCGTCATCAGGATCTTCAAGAAGGAGAACGGCGAGTT
CAAAATAGACTACGACAGAACTTTGAGCCATACATCTACGCGCTCTTGAAGGACGACTCTGCGATTGAGGACGTCA
AGAAGATAACTGCCGAGAGGCACGGCACTACCGTTAGGGTTGTCAGGGCCGAGAAAGTGAAGAAGAAGTTCTTAGGC
AGGCCGATAGAGGTCTGGAAGCTCTACTTCACTCACCCCCAGGACGTTCCCGCAATCAGGGACAAGATAAAGGAGCA
TCCTGCCGTTGTGGACATCTACGAGTACGACATCCCCCTCGCGAAGCGCTACCTCATAGACAAAGGCTTAATCCCGA
TGGAGGGCGACGAGGAACCTTAAGATGCTCGCCTTCGACATCGAGACGCTCTATCACGAGGGCGAGGAGTTCCGCCAA
GGGCTATCCTGATGATAAGCTACGCCGACGAGGAAGGGGCGCGCTTATTACCTGGAAGAATATCGACCTTCCCTA
TGTCGACGTCGTTTCCACCGAGAAGGAGATGATAAAGCGCTTCTCAAGGTCGTCAAGGAAAAGGATCCCGACGTCC
TCATAACCTACAACGGCGACAACCTTCGACTTCGCCTACCTCAAGAAGCGCTCCGAGAAGCTCGGAGTCAAGTTCATC
CTCGGAAGGGAAGGGAGCGAGCCGAAAATCCAGCGCATGGGCGATCGCTTTGCGGTGGAGGTCAAGGGAAGGATTCA
CTTCGACCTCTACCCCGTCATTAGGAGAACGATTAACTCCCACTTACACCTTGAGGCAGTATATGAAGCCATCT
TTGGACAGCCGAAGGAGAAGGTCTACGCTGAGGAGATAGCGCAGGCCTGGGAAACGGGCGAGGGATTAGAAAGGGTG
GCCCCGCTACTCGATGGAGGACGCAAAGGTAACCTATGAACTCGGAAAAGAGTTCTTCCCTATGGAAGCCCAGCTCTC
GCGCCTCGTAGGCCAGAGCCTCTGGGATGTATCTCGCTCGAGTACCGGAAACCTCGTCGAGTGGTTTTTGTCTGAGGA
AGGCCTACGAGAGGAATGAACCTTGACCAAAACAAGCCGACGAGAGGAGCTGGCAAGAAGAAGGGAGAGCTACGCG
GGTGGATACGTCAAGGAGCCCAGAAAGGGGACTGTGGGAGAACATCGTGATCTGGACTTCCGCTCCCTGTATCCTTC
GATAATAATCACCATAACGTCTCCCTGATACTCAACAGGGAGGGTTGTGAGGAGTACGACGTGGCTCCTCAGG
TAGGCCATAAGTTCTGCAAGGACTTCCCCGGCTTCATCCCAAGCCTCCTCGGAGACCTCTTGAGGAGAGACAGAAG
GTAAAGAAGAAGATGAAGGCCACTATAGACCCAATCGAGAAGAACTCCTCGATTACAGGCAACGAGCAATCAAAAT
CCTTGCTAATAGCTTCTACGGTTACTACGGCTATGCAAAGGCCCGCTGGTACTGCAAGGAGTGCGCCGAGAGCGTTA
CCGCTTGGGGCAGGCAGTACATCGAGACCACGATAAGGGAAATAGAGGAGAAATTTGGCTTTAAAGTCCTCTACGCG
GACACAGATGGATTTTTCGCAACAATACCTGGAGCGGACGCCGAAACCGTCAAAAAGAAGGCAAAGGAGTTCCTGGA
CTACATCAACGCCAACTGCCCGGCTGCTCGAACTCGAATACGAGGGCTTCTACAAGCGCGGCTTCTTCGTGACGA
AGAAGAAGTACGCGGTTATAGACGAGGAGGACAAGATAACGACGCGGGCTTGAAATAGTTAGGCGTGACTGGAGC
GAGATAGCGAAGGAGACGCGAGGCGAGGGTTCTTGAGGCGATACTAAAGCACGGTGACGTTGAAGAAGCGGTAAGGAT
TGTCAAAGAGGTTACGGAGAAGCTGAGCAAGTACGAGGTTCCACCGGAGAAGCTGGTCATCTACGAGCAGATAACCC
GCGACCTGAAGGACTACAAGGCCACCGGGCCGATGTGGCTGTTGCAAAACGCCTCGCCGCAAGGGGGATAAAAATC
CGGCCCCGAACGGTCATAAGCTACATCGTGCTCAAAGGCTCGGGAAGGATTGGGGACAGGGCTATACCTTTGACGA
ATTTGACCCGGCAAAGCACAAGTACGATGCAGAATACTACATCGAGAACCAGGTTCTTCCAGCTGTGGAGAGGATTC
TGAGGGCCTTTGGTTACCGTAAAGAAGATTTAAGGTATCAGAAAACGCGGCAGGTTGGCTTGGGGGCGTGGCTAAAA
CCTAAGACATGA

PFU DNA POLYMERASE (SEQ ID NO: 23)

G387P Mutant (CCN is the codon for Proline where N = C, G, A, or T)

V93R MUTANT: GTT CAN BE MODIFIED TO BE = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)

V93E MUTANT: GTT CAN BE MODIFIED TO BE = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)

V93D MUTANT: GTT CAN BE MODIFIED TO BE = GAT, GAC (ALL CODONS FOR ASPARTIC ACID)

V93K MUTANT: GTT CAN BE MODIFIED TO BE = AAA, AAG (ALL CODONS FOR LYSINE)

V93N MUTANT: GTT CAN BE MODIFIED TO BE = AAC, AAU (ALL CODONS FOR ASPARAGINE)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATGTTT CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAAGCTTG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCACTTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGATG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACACC NGGATTCGTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCTT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGAAGAAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATFACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTGCA 1860
AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328

PFU DNA POLYMERASE (SEQ ID NO: 24)
 D141A/E143A Mutant (GCN is the codon for alanine where N = C, G, A, or T)
 V93R MUTANT: GTT CAN BE MODIFIED TO BE = AGA, AGG, CGA, CGC, CGG, CGT (ALL POSSIBLE CODONS FOR ARGININE)
 V93E MUTANT: GTT CAN BE MODIFIED TO BE = GAA, GAG (ALL CODONS FOR GLUTAMIC ACID)
 V93D MUTANT: GTT CAN BE MODIFIED TO BE = GAT, GAC (ALL CODONS FOR ASPARTIC ACID)
 V93K MUTANT: GTT CAN BE MODIFIED TO BE = AAA, AAG (ALL CODONS FOR LYSINE)
 V93N MUTANT: GTT CAN BE MODIFIED TO BE = AAC, AAU (ALL CODONS FOR ASPARAGINE)

ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
 AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTACGCT 120
 CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
 AAGATTGTGA GAATTGTTGA TGTAAGAAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
 ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGATGTTT CCACTATTAG AGAAAAAGTT 300
 AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTCG AAAGAGATAC 360
 CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GCNATAGCNA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
 AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGA AAAACATAGA TCTTCCATAC 540
 GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
 AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
 AAAAGGGCAG AAAAAGCTTG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
 ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTCGACTTG 780
 TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
 GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
 AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
 GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCTAGCTT CAAGATTAGT TGGACAACCT 1020
 TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGATG AGTGGTTCTT ACTTAGGAAA 1080
 GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
 CTCAGGGAGA GCTACACAGG TGGATTGCTT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
 ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCA CAATGTTTCT 1260
 CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
 AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTG GTTAGAGGAA 1380
 AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
 GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATCTT TCTACGGATA TTATGGCTAT 1500
 GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTACTGCCTG GGAAGAAAAG 1560
 TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTAAAGT CCTCTACATT 1620
 GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
 GCTCTAGAAT TTGTAAAATA CATAAATTC AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
 GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
 GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAATTGCA 1860
 AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
 GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
 CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
 GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
 GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
 TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCCTCCA 2220
 GCGGTACTTA GGATATTGGA GGGATTGGA TACAGAAAGG AAGACCTCAG ATACCAAAAG 2280
 ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328

PFU DNA POLYMERASE (SEQ ID NO: 25)

V93 DELETION MUTANT

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ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAAGAT---C CCACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480
AGTTATGCAG ATGAAAATGA AGCAAAGGTG ATTACTTGGG AAAACATAGA TCTTCCATAC 540
GTTGAGGTTG TATCAAGCGA GAGAGAGATG ATAAAGAGAT TTCTCAGGAT TATCAGGGAG 600
AAGGATCCTG ACATTATAGT TACTTATAAT GGAGACTCAT TCGCATTCCC ATATTTAGCG 660
AAAAGGGCAG AAAAATTGGG GATTAAATTA ACCATTGGAA GAGATGGAAG CGAGCCCAAG 720
ATGCAGAGAA TAGGCGATAT GACGGCTGTA GAAGTCAAGG GAAGAATACA TTTGACTTGG 780
TATCATGTAA TAACAAGGAC AATAAATCTC CCAACATACA CACTAGAGGC TGTATATGAA 840
GCAATTTTTG GAAAGCCAAA GGAGAAGGTA TACGCCGACG AGATAGCAAA AGCCTGGGAA 900
AGTGGAGAGA ACCTTGAGAG AGTTGCCAAA TACTCGATGG AAGATGCAAA GGCAACTTAT 960
GAACTCGGGA AAGAATTCCT TCCAATGGAA ATTCAGCTTT CAAGATTAGT TGGACAACCT 1020
TTATGGGATG TTTCAAGGTC AAGCACAGGG AACCTTGTAG AGTGGTTCTT ACTTAGGAAA 1080
GCCTACGAAA GAAACGAAGT AGCTCCAAAC AAGCCAAGTG AAGAGGAGTA TCAAAGAAGG 1140
CTCAGGGAGA GCTACACAGG TGGATTTCGT AAAGAGCCAG AAAAGGGGTT GTGGGAAAAC 1200
ATAGTATACC TAGATTTTAG AGCCCTATAT CCCTCGATTA TAATTACCCA CAATGTTTCT 1260
CCCGATACTC TAAATCTTGA GGGATGCAAG AACTATGATA TCGCTCCTCA AGTAGGCCAC 1320
AAGTTCTGCA AGGACATCCC TGGTTTTATA CCAAGTCTCT TGGGACATTT GTTAGAGGAA 1380
AGACAAAAGA TTAAGACAAA AATGAAGGAA ACTCAAGATC CTATAGAAAA AATACTCCTT 1440
GACTATAGAC AAAAAGCGAT AAAACTCTTA GCAAATTCCT TCTACGGATA TTATGGCTAT 1500
GCAAAAGCAA GATGGTACTG TAAGGAGTGT GCTGAGAGCG TTAGTGCCTG GGGAAGAAAG 1560
TACATCGAGT TAGTATGGAA GGAGCTCGAA GAAAAGTTTG GATTTAAAGT CCTCTACATT 1620
GACACTGATG GTCTCTATGC AACTATCCCA GGAGGAGAAA GTGAGGAAAT AAAGAAAAAG 1680
GCTCTAGAAT TTGTAAATA CATAAATTCA AAGCTCCCTG GACTGCTAGA GCTTGAATAT 1740
GAAGGGTTTT ATAAGAGGGG ATTCTTCGTT ACGAAGAAGA GGTATGCAGT AATAGATGAA 1800
GAAGGAAAAG TCATTACTCG TGGTTTAGAG ATAGTTAGGA GAGATTGGAG TGAAATTGCA 1860
AAAGAACTC AAGCTAGAGT TTTGGAGACA ATACTAAAAC ACGGAGATGT TGAAGAAGCT 1920
GTGAGAATAG TAAAAGAAGT AATACAAAAG CTTGCCAATT ATGAAATTCC ACCAGAGAAG 1980
CTCGCAATAT ATGAGCAGAT AACAAGACCA TTACATGAGT ATAAGGCGAT AGGTCCTCAC 2040
GTAGCTGTTG CAAAGAAACT AGCTGCTAAA GGAGTTAAAA TAAAGCCAGG AATGGTAATT 2100
GGATACATAG TACTTAGAGG CGATGGTCCA ATTAGCAATA GGGCAATTCT AGCTGAGGAA 2160
TACGATCCCA AAAAGCACAA GTATGACGCA GAATATTACA TGGAGAACCA GGTTCTTCCA 2220
GCGGTACTTA GGATATTGGA GGGATTTGGA TACAGAAAGG AAGACCTCAG ATACCAAAG 2280
ACAAGACAAG TCGGCCTAAC TTCCTGGCTT AACATTAAAA AATCCTAG 2328

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PFU DNA POLYMERASE (SEQ ID NO: 26)

D92-V93-P94 DELETION MUTANT

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ATGATTTTAG ATGTGGATTA CATAACTGAA GAAGGAAAAC CTGTTATTAG GCTATTCAAA 60
AAAGAGAACG GAAAATTTAA GATAGAGCAT GATAGAACTT TTAGACCATA CATTTACGCT 120
CTTCTCAGGG ATGATTCAAA GATTGAAGAA GTTAAGAAAA TAACGGGGGA AAGGCATGGA 180
AAGATTGTGA GAATTGTTGA TGTAGAGAAG GTTGAGAAAA AGTTTCTCGG CAAGCCTATT 240
ACCGTGTGGA AACTTTATTT GGAACATCCC CAA ACTATTAG AGAAAAAGTT 300
AGAGAACATC CAGCAGTTGT GGACATCTTC GAATACGATA TTCCATTTGC AAAGAGATAC 360
CTCATCGACA AAGGCCTAAT ACCAATGGAG GGGGAAGAAG AGCTAAAGAT TCTTGCCTTC 420
GATATAGAAA CCCTCTATCA CGAAGGAGAA GAGTTTGGAA AAGGCCCAAT TATAATGATT 480

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AGTTATGCAG	ATGAAAATGA	AGCAAAGGTG	ATTACTTGGG	AAAACATAGA	TCTTCCATAC	540
GTTGAGGTTG	TATCAAGCGA	GAGAGAGATG	ATAAAGAGAT	TTCTCAGGAT	TATCAGGGAG	600
AAGGATCCTG	ACATTATAGT	TACTTATAAT	GGAGACTCAT	TCGCATTCCC	ATATTTAGCG	660
AAAAGGGCAG	AAAAACTTGG	GATTAAATTA	ACCATTGGAA	GAGATGGAAG	CGAGCCCAAG	720
ATGCAGAGAA	TAGGCGATAT	GACGGCTGTA	GAAGTCAAGG	GAAGAATACA	TTTCGACTTG	780
TATCATGTAA	TAACAAGGAC	AATAAATCTC	CCAACATACA	CACTAGAGGC	TGTATATGAA	840
GCAATTTTTG	GAAAGCCAAA	GGAGAAGGTA	TACGCCGACG	AGATAGCAAA	AGCCTGGGAA	900
AGTGGAGAGA	ACCTTGAGAG	AGTTGCCAAA	TACTCGATGG	AAGATGCAAA	GGCAACTTAT	960
GAACTCGGGA	AAGAATTCCT	TCCAATGGAA	ATTCAGCTTT	CAAGATTAGT	TGGACAACCT	1020
TTATGGGATG	TTTCAAGGTC	AAGCACAGGG	AACCTTGTA	AGTGGTTCTT	ACTTAGGAAA	1080
GCCTACGAAA	GAAACGAAGT	AGCTCCAAAC	AAGCCAAGTG	AAGAGGAGTA	TCAAAGAAGG	1140
CTCAGGGAGA	GCTACACAGG	TGGATTTCGT	AAAGAGCCAG	AAAAGGGGTT	GTGGGAAAAC	1200
ATAGTATACC	TAGATTTTAG	AGCCCTATAT	CCCTCGATTA	TAATTACCCA	CAATGTTTCT	1260
CCCATACTC	TAAATCTTGA	GGGATGCAAG	AACTATGATA	TCGCTCCTCA	AGTAGGCCAC	1320
AAGTTCTGCA	AGGACATCCC	TGGTTTTATA	CCAAGTCTCT	TGGGACATTT	GTTAGAGGAA	1380
AGACAAAAGA	TTAAGACAAA	AATGAAGGAA	ACTCAAGATC	CTATAGAAAA	AATACTCCTT	1440
GACTATAGAC	AAAAGCGAT	AAAACCTCTTA	GCAAATTCCT	TCTACGGATA	TTATGGCTAT	1500
GCAAAAGCAA	GATGGTACTG	TAAGGAGTGT	GCTGAGAGCG	TTACTGCCTG	GGGAAGAAAG	1560
TACATCGAGT	TAGTATGGAA	GGAGCTCGAA	GAAAAGTTTG	GATTTAAAGT	CCTCTACATT	1620
GACACTGATG	GTCTCTATGC	AACTATCCCA	GGAGGAGAAA	GTGAGGAAAT	AAAGAAAAAG	1680
GCTCTAGAAT	TTGTAAAATA	CATAAATTCA	AAGCTCCCTG	GAATGCTAGA	GCTTGAATAT	1740
GAAGGGTTTT	ATAAGAGGGG	ATTCTTCGTT	ACGAAGAAGA	GGTATGCAGT	AATAGATGAA	1800
GAAGGAAAAG	TCATTACTCG	TGGTTTAGAG	ATAGTTAGGA	GAGATTGGAG	TGAAATTGCA	1860
AAAGAACTC	AAGCTAGAGT	TTTGGAGACA	ATACTAAAAC	ACGGAGATGT	TGAAGAAGCT	1920
GTGAGAATAG	TAAAAGAAGT	AATACAAAAG	CTTGCCAATT	ATGAAATTCC	ACCAGAGAAG	1980
CTCGCAATAT	ATGAGCAGAT	AACAAGACCA	TTACATGAGT	ATAAGGCGAT	AGGTCCCTCAC	2040
GTAGCTGTTG	CAAAGAACT	AGCTGCTAAA	GGAGTTAAAA	TAAAGCCAGG	AATGGTAATT	2100
GGATACATAG	TACTTAGAGG	CGATGGTCCA	ATTAGCAATA	GGGCAATTCT	AGCTGAGGAA	2160
TACGATCCCA	AAAAGCACAA	GTATGACGCA	GAATATTACA	TGGAGAACCA	GGTTCTTCCA	2220
GCGGTACTTA	GGATATTGGA	GGGATTTGGA	TACAGAAAGG	AAGACCTCAG	ATACCAAAAG	2280
ACAAGACAAG	TCGGCCTAAC	TTCCTGGCTT	AACATTAAAA	AATCCTAG	2328	

Figure 6B

>Pfu (SEQ ID NO: 27)

VALINE AT POSITION 93 MAY BE SUBSTITUTED BY ONE OF: R, E, D, K, OR N

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDS KIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDVPTIREKVVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDL PYVEVVSSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TGGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQAKIKLLANSFYGYGYAKARWYCKEAEVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEIEKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEEDPKKHKYDAEYYIENQVLPVLRILEGFGYRKEDLRYQKTRQVGLTSLW
NIKKS

>DEEP VENT (SEQ ID NO: 28)

VALINE AT POSITION 93 MAY BE SUBSTITUTED BY ONE OF: R, E, D, K, Q, OR N

MILDADYITEDGKPIIRIFKKENGFEKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHGKIVRIIDAEKVRKKFLG
RPIEVWRLYFEHPQDVPAIRDKIREHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAK
GPIIMISYADEEEAKVITWKKIDL PYVEVVSSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLVKRAEKLGIKLP
LGRDGSEPKMQRLGDMTAVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKKEKVYAHEIAEAWETGKGLERV
AKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSTGNLVEWYLLRKAYERNELAPNKPDEREYERRLRESY
AGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFKCDFPGFIPSLLRLLDERQ
EIKRKMKASKDPIEKKMLDYRQRAIKILANSYGYGYAKARWYCKEAEVTAWGREYIEFVRKELEEKFGFKVLY
IDTDGLYATIPGAKPEEIKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLIVRRDW
SEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIEYEQITRPLHEYKAIGPHVAVAKRLAARGVK
VRPGMVIGYIVLRGDGPISKRAILAEEDLRKHKYDAEYYIENQVLPVLRILEAFGYRKEDLRWQTKQTGLTAWL
NIKKK

>TGO (SEQ ID NO: 29)

VALINE AT POSITION 93 MAY BE SUBSTITUTED BY ONE OF: R, E, D, K, Q, OR N

MILDTDYITEDGKPVIRIFKKENGFEKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTRVVRVRAEKVKKKFLG
RPIEVWKLYFTHPQDVPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAE
GPILMISYADEEGARVITWKNIDL PYVDVVSSTEKEMIKRFLKVVKEDPDVLITYNGDNFDFAYLKKRSEKLGVKFI
LGREGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKKEKVYAEIEAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDERELARRRESYA
GGYVKEPERGLWENIVYLDLFRSLYPSIIITHNVSPDTLNREGCEEYDVAQVGHKFKCDFPGFIPSLLGDLLEERQK
VKKMKMATIDPIEKKLLDYRQRAIKILANSFYGYGYAKARWYCKEAEVTAWGRQYIETTIREIEEKFGFKVLYA

DTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWS
EIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIEQITRDLKDYKATGPHVAVAKRLAARGIKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLPAPERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKT

>KOD (SEQ ID NO: 30)

VALINE AT POSITION 93 MAY BE SUBSTITUTED BY ONE OF: R, E, D, K, Q, OR N

MILDTDYITEDGKPVIRIFKKENGFEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLG
RPVEVWKLIFYTHPQDVPAIRDKIREHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGEEFAE
GPILMISYADEEGARVITWKNVDLPYVDVSTEREMIKRFLRVVKEKDPDLITYNGDNFDFAYLKKRCEKLGINF
LGRDGSEPKIQRMGDRFAVEVKGRIFDLYPVIRRTINLPTYTLEAVYEAVFGQPKEKVYAEIITPAWETGENL
ARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYE
GGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHFCKDFPGFIPSLGDLLEERQK
IKKKMKATIDPIERKLLDYRQRAIKILANSYYGYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYS
DTDGFFATIPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEALLKGDGVEKAVRIVKEVTEKLSKYEVPPEKLVIEHQITRDLKDYKATGPHVAVAKRLAARGVKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLPAPERILRAFGYRKEDLRYQKTRQVGLSAWLK
PKGT

>VENT (SEQ ID NO: 31)

VALINE AT POSITION 93 MAY BE SUBSTITUTED BY ONE OF: R, E, D, K, Q, OR N

MILDTDYITKDGKPIIRIFKKENGFEFKIELDPHFQPYIYALLKDDSAIEEIKAIKGERHKGKTVRVLDAVKVRKKFLG
REVEVWKLIFEHPQDVPAAMRGKIREHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGDEFGK
GEIIMISYADEEEARVITWKNIDLDPYVDVVSNEREMIKRFVQVVKEKDPDVIITYNGDNFDPYLIKRAEKLGVRLV
LGRDKEHPEPKIQRMGDSFAVEIKGRIFDLFPVVRTINLPTYTLEAVYEAVLGKTKSKLGAEIEIAAIWETEESMK
KLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSTGNLVEWYLLRVAYARNELAPNKPDEEYKRRRLRT
TYLGGYVKEPEKGLWENIYLDFRSLYPSIIIVTHNVSPDTLEKEGCKNYDVAPIVGYRFCKDFPGFIPSLGDLIAM
RQDIKKMKSTIDPIEKKMLDYRQRAIKLLANSYYGYMGYPKARWYSKECAESVTAWGRHYIEMTIREIEEKFGFKV
LYADTDGFYATIPGEKPELIKKAKEFLNYINSLKPLGLLELEYEGFYLRGFFVTKKRYAVIDEEGRITTRGLEVVRR
DWSEIAKETQAKVLEAILKEGSVEKAVEVVRDVVEKIAKYRVPLEKLVIEHQITRDLKDYKAIGHVAIAKRLAARG
IKVKPGTIISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYIENQVLPALVRILEAFGYRKEDLRYQSSKQTGLDA
WLKR

>JDF-3 (SEQ ID NO: 32)

VALINE AT POSITION 93 MAY BE SUBSTITUTED BY ONE OF: R, E, D, K, Q, OR N

MILDVDYITENGKPVIRVFKKENGFEFRIEYDREFEPYFYALLRDDSIAIEEIKKITAERHGRVVKVRAEKVKKKFLG
RSVEVWVLYFTHPQDVPAIRDKIRKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLMSFDIETLYHEGEEFGT
GPILMISYADESEARVITWKKIDLPHYEVVSTEKEMIKRFLRVVKEKDPDLITYNGDNFDFAYLKKRCEKLGVSFT
LGRDGSEPKIQRMGDRFAVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKKEKVYAEIATAWETGEGLERV
ARYSMEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSTGNLVEWFLLRKAYERNELAPNKPDERELARRRGYA
GGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAVEVGHKFKCKDFPGFIPSLGNLLEERQK
IKKKMKATLDPLEKNLLDYRQRAIKILANSYYGYGYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYA
DTDGLHATIPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWS
EIAKETQARVLEAILRHGDVEEAVRIVREVTEKLSKYEVPPEKLVIEHQITRELKDYKATGPHVAIAKRLAARGVKI
RPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDADYYIENQVLPAPERILRAFGYRKEDLRYQKTRQVGLGAWLK
PKGKKK

>Pfu V93/G387P (SEQ ID NO: 33)

VALINE AT POSITION 93 MAY BE SUBSTITUTED BY ONE OF: R, E, D, K, OR N

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPHYVEVSSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAI FGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TPGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVLRILEGFGYRKEDLRYQKTRQVGLTSLW
NIKKS

>Pfu V93/D141A/E143A (SEQ ID NO: 34)

VALINE AT POSITION 93 MAY BE SUBSTITUTED BY ONE OF: R, E, D, K, OR N

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
GPIIMISYADENEAKVITWKNIDLPHYVEVSSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
IGRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAI FGKPKEKVYADEIAKAWESGENLERV
AKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
TGGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQ
KIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
IDTDGLYATIPGGESEEEIKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIVRRDW
SEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVLRILEGFGYRKEDLRYQKTRQVGLTSLW
NIKKS

>Pfu delta V93 (SEQ ID NO: 35)

MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGK
PIIMISYADENEAKVITWKNIDLPHYVEVSSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLT
GRDGSEPKMQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAI FGKPKEKVYADEIAKAWESGENLERV
KYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRLRESY
GGFVKEPEKGLWENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPGFIPSLLGHLLEERQ
IKTKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLY
DTDGLYATIPGGESEEEIKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLIVRRDWS
EIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVK
IKPGMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVLRILEGFGYRKEDLRYQKTRQVGLTSLW
IKKS //

>Pfu delta D92-V93-P94 (SEQ ID NO: 36)

MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDS KIEEVKKITGERHGKIVRIVDVEKVEKKFLG
KPITVWKLYLEHPQTIREKVREHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGEEFGKGPI
IMISYADENEAKVITWKNIDL PYVEVVSSEMIKRFRLRIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLTIGR
DGSEPKMQRIGDMTAVEVKGRIFDLYHVITRTINLPTYTLEAVYEAI FGKPKEKVYADEIAKAWESGENLERVAKY
SMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSSTGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRESYTGG
FVKEPEKGLWENIVYLD FRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSL LGHLL EERQKIK
TKMKETQDPIEKILLDYRQKAIKLLANSFYGYGYAKARWYCKEAE SVTAWGRKYIELVWKELEEKFGFKVLYIDT
DGLYATIPGGESEEEKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEIVRRDWSEI
AKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKKLAAGVKIKP
GMVIGYIVLRGDGPISNRAILAEYDPKKHKYDAEYYIENQVLPVLRILEGFGYRKEDLRYQKTRQVGLTSWLNK
KS >Pfu

Figure 6C-1 (SEQ ID NOS: 37[nt] and 38[aa])

5'

atg atc ctc gat aca gac tac ata act gag gat gga aag ccc gtc atc 48

Met Ile Leu Asp Thr Asp Tyr Ile Thr Glu Asp Gly Lys Pro Val Ile

1 5 10 15

agg atc ttc aag aag gag aac ggc gag ttc aaa ata gac tac gac aga 96

Arg Ile Phe Lys Lys Glu Asn Gly Glu Phe Lys Ile Asp Tyr Asp Arg

20 25 30

aac ttt gag cca tac atc tac gcg ctc ttg aag gac gac tct gcg att 144

Asn Phe Glu Pro Tyr Ile Tyr Ala Leu Leu Lys Asp Asp Ser Ala Ile

35 40 45

gag gac gtc aag aag ata act gcc gag agg cac ggc act acc gtt agg 192

Glu Asp Val Lys Lys Ile Thr Ala Glu Arg His Gly Thr Thr Val Arg

50 55 60

gtt gtc agg gcc gag aaa gtg aag aag aag ttc cta ggc agg ccg ata 240

Val Val Arg Ala Glu Lys Val Lys Lys Lys Phe Leu Gly Arg Pro Ile

65 70 75 80

gag gtc tgg aag ctc tac ttc act cac ccc cag gac nnn ccc gca atc 288

Glu Val Trp Lys Leu Tyr Phe Thr His Pro Gln Asp Xaa Pro Ala Ile

85 90 95

agg gac aag ata aag gag cat cct gcc gtt gtg gac atc tac gag tac 336

Arg Asp Lys Ile Lys Glu His Pro Ala Val Val Asp Ile Tyr Glu Tyr	
100	105
110	
gac atc ccc ttc gcg aag cgc tac ctc ata gac aaa ggc tta atc ccg	384
Asp Ile Pro Phe Ala Lys Arg Tyr Leu Ile Asp Lys Gly Leu Ile Pro	
115	120
125	
atg gag ggc gac gag gaa ctt aag atg ctc gcc ttc gac atc gag acg	432
Met Glu Gly Asp Glu Glu Leu Lys Met Leu Ala Phe Asp Ile Glu Thr	
130	135
140	
ctc tat cac gag ggc gag gag ttc gcc gaa ggg cct atc ctg atg ata	480
Leu Tyr His Glu Gly Glu Glu Phe Ala Glu Gly Pro Ile Leu Met Ile	
145	150
155	160
agc tac gcc gac gag gaa ggg gcg cgc gtt att acc tgg aag aat atc	528
Ser Tyr Ala Asp Glu Glu Gly Ala Arg Val Ile Thr Trp Lys Asn Ile	
165	170
175	
gac ctt ccc tat gtc gac gtc gtt tcc acc gag aag gag atg ata aag	576
Asp Leu Pro Tyr Val Asp Val Val Ser Thr Glu Lys Glu Met Ile Lys	
180	185
190	
cgc ttc ctc aag gtc gtc aag gaa aag gat ccc gac gtc ctc ata acc	624
Arg Phe Leu Lys Val Val Lys Glu Lys Asp Pro Asp Val Leu Ile Thr	
195	200
205	
tac aac ggc gac aac ttc gac ttc gcc tac ctc aag aag cgc tcc gag	672

Tyr Asn Gly Asp Asn Phe Asp Phe Ala Tyr Leu Lys Lys Arg Ser Glu	
210	215
	220
aag ctc gga gtc aag ttc atc ctc gga agg gaa ggg agc gag ccg aaa	720
Lys Leu Gly Val Lys Phe Ile Leu Gly Arg Glu Gly Ser Glu Pro Lys	
225	230
	235
	240
atc cag cgc atg ggc gat cgc ttt gcg gtg gag gtc aag gga agg att	768
Ile Gln Arg Met Gly Asp Arg Phe Ala Val Glu Val Lys Gly Arg Ile	
245	250
	255
cac ttc gac ctc tac ccc gtc att agg aga acg att aac ctc ccc act	816
His Phe Asp Leu Tyr Pro Val Ile Arg Arg Thr Ile Asn Leu Pro Thr	
260	265
	270
tac acc ctt gag gca gta tat gaa gcc atc ttt gga cag ccg aag gag	864
Tyr Thr Leu Glu Ala Val Tyr Glu Ala Ile Phe Gly Gln Pro Lys Glu	
275	280
	285
aag gtc tac gct gag gag ata gcg cag gcc tgg gaa acg ggc gag gga	912
Lys Val Tyr Ala Glu Glu Ile Ala Gln Ala Trp Glu Thr Gly Glu Gly	
290	295
	300
tta gaa agg gtg gcc cgc tac tcg atg gag gac gca aag gta acc tat	960
Leu Glu Arg Val Ala Arg Tyr Ser Met Glu Asp Ala Lys Val Thr Tyr	
305	310
	315
	320
gaa ctc gga aaa gag ttc ttc cct atg gaa gcc cag ctc tcg cgc ctc	1008

Glu Leu Gly Lys Glu Phe Phe Pro Met Glu Ala Gln Leu Ser Arg Leu
325 330 335

gta ggc cag agc ctc tgg gat gta tct cgc tcg agt acc gga aac ctc 1056

Val Gly Gln Ser Leu Trp Asp Val Ser Arg Ser Ser Thr Gly Asn Leu
340 345 350

gtc gag tgg ttt ttg ctg agg aag gcc tac gag agg aat gaa ctt gca 1104

Val Glu Trp Phe Leu Leu Arg Lys Ala Tyr Glu Arg Asn Glu Leu Ala
355 360 365

cca aac aag ccg gac gag agg gag ctg gca aga aga agg gag agc tac 1152

Pro Asn Lys Pro Asp Glu Arg Glu Leu Ala Arg Arg Arg Glu Ser Tyr
370 375 380

gcg ggt gga tac gtc aag gag ccc gaa agg gga ctg tgg gag aac atc 1200

Ala Gly Gly Tyr Val Lys Glu Pro Glu Arg Gly Leu Trp Glu Asn Ile
385 390 395 400

gtg tat ctg gac ttc cgc tcc ctg tat cct tcg ata ata atc acc cat 1248

Val Tyr Leu Asp Phe Arg Ser Leu Tyr Pro Ser Ile Ile Ile Thr His
405 410 415

aac gtc tcc cct gat aca ctc aac agg gag ggt tgt gag gag tac gac 1296

Asn Val Ser Pro Asp Thr Leu Asn Arg Glu Gly Cys Glu Glu Tyr Asp
420 425 430

gtg gct cct cag gta ggc cat aag ttc tgc aag gac ttc ccc ggc ttc 1344

Val Ala Pro Gln Val Gly His Lys Phe Cys Lys Asp Phe Pro Gly Phe

435

440

445

atc cca agc ctc ctc gga gac ctc ttg gag gag aga cag aag gta aag 1392

Ile Pro Ser Leu Leu Gly Asp Leu Leu Glu Glu Arg Gln Lys Val Lys

450

455

460

aag aag atg aag gcc act ata gac cca atc gag aag aaa ctc ctc gat 1440

Lys Lys Met Lys Ala Thr Ile Asp Pro Ile Glu Lys Lys Leu Leu Asp

465

470

475

480

tac agg caa cga gca atc aaa atc ctt gct aat agc ttc tac ggt tac 1488

Tyr Arg Gln Arg Ala Ile Lys Ile Leu Ala Asn Ser Phe Tyr Gly Tyr

485

490

495

tac ggc tat gca aag gcc cgc tgg tac tgc aag gag tgc gcc gag agc 1536

Tyr Gly Tyr Ala Lys Ala Arg Trp Tyr Cys Lys Glu Cys Ala Glu Ser

500

505

510

gtt acc gct tgg ggc agg cag tac atc gag acc acg ata agg gaa ata 1584

Val Thr Ala Trp Gly Arg Gln Tyr Ile Glu Thr Thr Ile Arg Glu Ile

515

520

525

gag gag aaa ttt ggc ttt aaa gtc ctc tac gcg gac aca gat gga ttt 1632

Glu Glu Lys Phe Gly Phe Lys Val Leu Tyr Ala Asp Thr Asp Gly Phe

530

535

540

ttc gca aca ata cct gga gcg gac gcc gaa acc gtc aaa aag aag gca 1680

Phe Ala Thr Ile Pro Gly Ala Asp Ala Glu Thr Val Lys Lys Lys Ala

545 550 555 560

aag gag ttc ctg gac tac atc aac gcc aaa ctg ccc ggc ctg ctc gaa 1728

Lys Glu Phe Leu Asp Tyr Ile Asn Ala Lys Leu Pro Gly Leu Leu Glu

565 570 575

ctc gaa tac gag ggc ttc tac aag cgc ggc ttc ttc gtg acg aag aag 1776

Leu Glu Tyr Glu Gly Phe Tyr Lys Arg Gly Phe Phe Val Thr Lys Lys

580 585 590

aag tac gcg gtt ata gac gag gag gac aag ata acg acg cgc ggg ctt 1824

Lys Tyr Ala Val Ile Asp Glu Glu Asp Lys Ile Thr Thr Arg Gly Leu

595 600 605

gaa ata gtt agg cgt gac tgg agc gag ata gcg aag gag acg cag gcg 1872

Glu Ile Val Arg Arg Asp Trp Ser Glu Ile Ala Lys Glu Thr Gln Ala

610 615 620

agg gtt ctt gag gcg ata cta aag cac ggt gac gtt gaa gaa gcg gta 1920

Arg Val Leu Glu Ala Ile Leu Lys His Gly Asp Val Glu Glu Ala Val

625 630 635 640

agg att gtc aaa gag gtt acg gag aag ctg agc aag tac gag gtt cca 1968

Arg Ile Val Lys Glu Val Thr Glu Lys Leu Ser Lys Tyr Glu Val Pro

645 650 655

ccg gag aag ctg gtc atc tac gag cag ata acc cgc gac ctg aag gac 2016

Pro Glu Lys Leu Val Ile Tyr Glu Gln Ile Thr Arg Asp Leu Lys Asp

660

665

670

tac aag gcc acc ggg ccg cat gtg gct gtt gca aaa cgc ctc gcc gca 2064

Tyr Lys Ala Thr Gly Pro His Val Ala Val Ala Lys Arg Leu Ala Ala

675

680

685

agg ggg ata aaa atc cgg ccc gga acg gtc ata agc tac atc gtg ctc 2112

Arg Gly Ile Lys Ile Arg Pro Gly Thr Val Ile Ser Tyr Ile Val Leu

690

695

700

aaa ggc tcg gga agg att ggg gac agg gct ata ccc ttt gac gaa ttt 2160

Lys Gly Ser Gly Arg Ile Gly Asp Arg Ala Ile Pro Phe Asp Glu Phe

705

710

715

720

gac ccg gca aag cac aag tac gat gca gaa tac tac atc gag aac cag 2208

Asp Pro Ala Lys His Lys Tyr Asp Ala Glu Tyr Tyr Ile Glu Asn Gln

725

730

735

gtt ctt cca gct gtg gag agg att ctg agg gcc ttt ggt tac cgt aaa 2256

Val Leu Pro Ala Val Glu Arg Ile Leu Arg Ala Phe Gly Tyr Arg Lys

740

745

750

gaa gat tta agg tat cag aaa acg cgg cag gtt ggc ttg ggg gcg tgg 2304

Glu Asp Leu Arg Tyr Gln Lys Thr Arg Gln Val Gly Leu Gly Ala Trp

755

760

765

cta aaa cct aag aca tga 2322

Leu Lys Pro Lys Thr

Tgo93 (R): nnn = AGA, AGG, CGA, CGC, CGG, CGT (R)

Tgo 93 (R) amino acid sequence

Tgo 93 (E): nnn = GAA, GAG (E)

Tgo 93 (E) amino acid sequence

Tgo93 (D): nnn = GAT, GAC (D)

Tgo 93 (D) amino acid sequence

Tgo93 (K): nnn = AAA, AAG (K)

Tgo 93 (K) amino acid sequence

Tgo93 (Q): nnn = CAA, CAG (Q)

Tgo 93 (Q) amino acid sequence

Tgo93 (N): nnn = AAC, AAU (N)

Tgo 93 (N) amino acid sequence

Figure 7A

ACCESSION AAA72101 Vent Thermococcus litoralis

mildtdyitk dgkpiirifk kengefkiel dphfqpyiya llkddsaiee ikaikgerhg ktrrvldavk vrkkflgrev
evwklifehp qdvpamrgki rehpavvdiy eydipfakry lidkglipme gdeelklaf dietfyhegd efgkgeiimi
syadeearv itwknidlpv vdvvsnerem ikrfvqvve kdpdviityn gdnfdlpyli kraeklgvrl vlgrdkehpe
pkiqrmgdsf aveikgrihf dlfpvvrtri nlptyleav yeavlgkts klgaeeiaai weteesmkkl aqysmedara
tyelgkeffp meaelaklig qsvwdvsrss tgnlvewyll rvayarnela pnkpdeeeyk rrlrttylgg yvkepekglw
eniilydfis lypsiiivthn vspdtlekeg cknvdvapiy gyrfckdfpg fipsilgdli amrqdikkkm kstidpiekk
mldyrqraik llansyygym gypkarwysk ecaesvtawg rhyiemtire ieekfgfkvl yadtdgfyat ipgekelik
kkakeflnyi nsklpgllei eyegfylrgf fvtkkryavi deegrittrg levvrdwse iaketqakvl eailkegsve
kavevrvdvv ekiakyrvpv eklviheqit rdlkdykaig phvaiaakra argikvkgpt iisyivlkgk gkisdrvill
teydrkhky dpdyienqv lpavlrilea fgyrkedlry qsskqtglda wlkr (SEQ ID NO. 83)

ACCESSION O33845 THEST THERMOCOCCUS SP.

mildtdyitk dgkpiirifk kengefkiel dphfqpyiya llkddsaide ikaikgerhg kivrvvdavk vkkklgrdv
evwklifehp qdvpalrgki rehpavidiy eydipfakry lidkglipme gdeelklmaf dietfyhegd efgkgeiimi
syadeearv itwknidlpv vdvvsnerem ikrfvqvire kdpdvlityn gdnfdlpyli kraeklgvtl llgrdkehpe
pkihrmgdsf aveikgrihf dlfpvvrtri nlptyleav yeavlgkts klgaeeiaai weteesmkkl aqysmedara
tyelgkeffp meaelaklig qsvwdvsrss tgnlvewyll rvayarnela pnkpdeeeyr rrlrttylgg yvkeperglw
eniayldfrc hpadtkvivk gkgivnisdv kegdyilgid gwqrvkkvwk yhyegklini ngkctpnhk vpvvtendrq
trirdslaks flsgkvkgki ittklfekia efeknpsee eilkgelsgi ilaegtllrk dieyfdssrg kkrishqyrv eitigeneke
llerilyifd klfgirpsvk kkgdtnalki ttakkavylq ieellknies lyapavlrfg ferdatvnki rstivvtqgt nnkwkidiva
klldslgipy sryeykyien gkeltkhile itgrdglilf qtlvgfisse knealekaie vremenrlknn sfynlstfev
sseykgevy dltlegnpvy fangilthns lypsiivthn vspdtlerg cknvdvapiy gyrfckdfpg fipsilgeli
tmrqiakkkm katidpiekk mldyrqravk llansilpne wlpiiengev kfvkigefid rymeeqkdkv rtdvntevle
vdnifafsln keskkseikk vkalirhkyk geayevelns grkihitrgh slftirngki keiwgeevkv gdliivpkkv
knekeavin ipelisklpd edtadvvmtt pvkgrknffk gmlrtlkwif geeskirtf nrylfhleel gfvklprgy
evtdweglkr yrqlyeklvk nlryngnkre ylvrfndikd svscfprkel eewkigtgkg frxkcilkvd edfgkflgyy
vsegyagaqk nktggmsysv klynenpnvl kdmkniaekf fgkvrvgknc vdipkkmayl laksicgvta enkripsiif
dssepvrwaf lrayfvgdgd ihpskrlrls tksellanql vflnslgvs sikigfdsgv yrvyinedlp flqtsrqknt
yypnlipkev leeifgrkfq knitfekfke ladsgklidr kvklldfiln gdivldrvkn vekreyegyv ydlsvednen
flvgfgllia hnsyygymgy pkarwyskec aesvtawgrh yiemtikeie ekfgfkvlva dsvtgdteii vkngriefv
pieklfervd yrigekeyci ledvealtld nrgkliwkkv pyvmhrakk kvyriwitns wyidvtedhs livaedglke
arpmeiegks liatkddlsq veyikphaie eisyngyvyd ievgthrff angilvhntd gfyatipgek petikkkake
flkyinsklp glleleyegf ylgffvakk ryavideegr ittrglevvr rdwseiaket qakvleailk edsvekavei
vkdvveeiak yqvpleklvi heqitkdlse ykaighphvai akrlaakgik vrpgtiisiyi vlrgsgkisd rvillseydp
kkhkydpdyi ienqvlpavl rileafgyrk edlkyqsskq vglawlk (SEQ ID NO. 84)

ACCESSION P77916 Pab Pyrococcus abyssi

miidadyite dgkpiirifk kekgefkev dtrfpyiya llkddsaide vkkitaerhg kivritevek vqkkflgrpi evwklylehp qdvpaireki rehpavvdif eydipfakry lidkgltpme gneeltflav dietlyhege efgkgpiimi syadeegakv itwksidlpv vevvsserem ikrivkvire kdpdviityn gdnfdfpvll kraeklgikl plgrdnsepk mqrmgdsrav eikgrihfdl fpvirrtinl ptytleavve aifgkskekv yaheiaeawe tgkglervak ysmedakvtf elgkeffpme aqlarlvqqp vwdvsrsstg nlvewflrk ayernelapn kpdereyerr lresyeggyv kepekgweg ivsldfrsly psiiithnvs pdtlnrenck eydvapqvgf rfckdfpgfi psllgnlee rqkikkrmk skdpvekkll dyrqraikil ansyygygyg akarwyckec aesvtawgrq yidlvrrle srgfkvlyid tdglyatipg akheeikeka lkvveyinsk lpglleleye gfyargffvt kkyalidee gkivtrglei vrrdwseia etqakvleai lkhgnvdeav kivkevtel skyeppekl viyeqitrpl seykaigphv avakraakg vkvkpgmvig yivlrgdgp skraiaieef dpkhhkydae yyienqvlpa verilrafgy rkedlryqkt kvqglgawlk f (SEQ ID NO. 85)

ACCESSION O59610 PYRHO *Pyrococcus horikoshii*

mildadyite dgkpiirifk kengefkvey dtrfpyiya llrddsaide ikkitaqrhg kvvriretev iqrkflgrpi evwklylehp qdvpairedi rehpavvdif eydipfakry lidkgltpme gneeltflav dietlyhege efgkgpvimi syadeegakv itwkkidlpv vevvsserem ikrivvike kdpdviityn gdnfdfpvll kraeklgikl llgrdnsepk mqrmgdsrav eikgrihfdl fpvirrtinl ptytleavve aifgkpekv yadeiakawe tgeglervak ysmedakvty elgreffpme aqlarlvqqp vwdvsrsstg nlvewflrk ayernelapn kpdekeyerr lresyeggyv kepekgweg ivsldfrsly psiiithnvs pdtlnregce eydvapkvgh rfckdfpgfi psllgqlee rqkikkrmk skdpvekkll dyrqraikil ansilpdewl pivenekvrf vkigdfidre ieenaervkr dgeteilevk dlkalsfnre tkkselkkvk alirhrysgk vysiklksgr rikitsghsl fsvkngklvk vrgdelkpgd lvvpgrkl peskvlnlv ellklpeee tsnivmmipv kgrknffkgm lktlywifge gerprtagry lkhlerlgyv klrrgcevl dweslkryrk lyetliknlk yngnsraymv efnsldrvs lmpieelkew iigepgpk gtfidvdsf akllgyyiss gdvekdvrkf hskdqnvled iaklaeklfq kvrrrgyie vsgkishaif rvlaegkrip efiftspmdi kvafkglng naeltfstk sellvnqll llnsigvsdi kiehekgvyr vyinkkessn gdivdsves ievkyeggyv ydsvednen flvgfllly hnsyygygyg akarwyckec aesvtawgrq yidlvrrle argfkvlyid tdglyatipg vkdwveevkr alefvyins klpgvleley egfyargffv tkkkyalide egkivtrgle ivrrdwseia ketqarvlea ilkhgnveea vkivkdvtel ltnyevppek lviyeqitrp ineykaigph vavakrlmar gikvpgmvi gyivlrgdgp iskraisiee fdprkhkyda eyyenqvlpa averilkafg ykredlrwqk tkqvlgawi kvkks (SEQ ID NO. 86)

ACCESSION P77932 PYRSE *PYROCOCCUS* SP.

miidadyite dgkpiirifk kekgefkev dtrfpyiya llkddsaide vkkitaerhg kivritevek vqkkflgrpi evwklylehp qdvpaireki rehpavvdif eydipfakry lidkgltpme gneeltflav dietlyhege efgkgpiimi syadeegakv itwksidlpv vevvsserem ikrivkvire kdpdviityn gdnfdfpvll kraeklgikl plgrdnsepk mqrmgdsrav eikgrihfdl fpvirrtinl ptytleavve aifgkskekv yaheiaeawe tgkglervak ysmedakvtf elgkeffpme aqlarlvqqp vwdvsrsstg nlvewflrk ayernelapn kpdereyerr lresyeggyv kepekgweg ivsldfrsly psiiithnvs pdtlnrenck eydvapqvgf rfckdfpgfi psllgnlee rqkikkrmk skdpvekkll dyrqraikil ansyygygyg akarwyckec aesvtawgrq yidlvrrle ssgfkvlyid tdglyatipg akpneikeka lkvveyinsk lpglleleye gfyargffvt kkyalidee gkivtrglei vrrdwseia etqakvleai lkhgnvdeav kivkevtel skyeppekl viyeqitrpl seykaigphv avakraakg vkvkpgmvig yivlrgdgp skraiaieef dpkhhkydae yyienqvlpa verilrafgy rkedlryqkt kvqglgawlk f (SEQ ID NO. 87)

ACCESSION AAA67131 DeepVent Pyrococcus sp.

mildadyite dgkpiirfk kengefkvey dnmfrpyiya llkddsqide vrkitaerhg kivriidaek vrkkflgrpi
evwrlyfehp qdvpairedki rehsavidif eydipfakry lidkglipme gdeelklaf dietlyhege efakgpiimi
syadeeeakv itwkkidlpv vevvsserem ikrflkvire kdpdviityn gdsfdlpvlv kraeklgikl plgrdgsepk
mqrlgdmav eikgrihfdl yhvrrtinl ptytleavve aifgkpkkev yaheiaewe tgkglervak ysmedakvty
elgreffpme aqlsrlvgqp lwdvsrsstg nlvewyllrk ayernelapn kpdereyerr lresyaggyv kepekglweg
lvslldfrsly psiiithnvs pdtlnregcr eydvapevgh kfckdfpgfi psllkrllde rqeikrkmka skdpiekkml
dyrqaikil ansyygygygy akarwyckec aesvtawgre yiefvrkele ekfgfkvlyi dtdglyatip gakpeeikkk
alefvdya klpglleley egfyvrgffv tkkkyalide egkiitrgle ivrrdwseia ketqakvlea ilkhgnveea
vkivkevtek lskyeippe kviyeqitp lheykaighp vavaklaar gvkvrpgmvi gyivlrgdgp iskrailae
fdlrkhkyda eyyienqvlp avlrileafg yrkedlrwqk tkqgtltawl nikkk (SEQ ID NO. 88)

ACCESSION P80061 Pfu Pyrococcus furiosus

mildvdyite egkpvirfk kengfkfieh drtfrpyiya llrddskiee vkkitgerhg kivrivdvek vekkflgkpi
tvwkllyehp qdvptirekv rehpaavdif eydipfakry lidkglipme geeelkilaf dietlyhege efgkpiimi
syadeneakv itwknidlpv vevvsserem ikrflriire kdpdiityn gdsfdpyla kraeklgikl tigrdgsepk
mqrigdmav evkgrihfdl yhvrrtinl ptytleavve aifgkpkkev yadeiakawe sgenlervak ysmedakaty
elgkeflpme iqlsrlvgqp lwdvsrsstg nlvewflrk ayernevapn kpseeeyqrr lresytggfv kepekglwen
ivyldfraly psiiithnvs pdtlnlegck nydiapqvgf kfckdipgfi psllghlee rqkiktkmke tqdpickill
dyrqkaikil ansfygygygy akarwyckec aesvtawgrk yielvwkele ekfgfkvlyi dtdglyatip ggeseeikkk
alefvkyins klpglleley egfykrffv tkkryavide egkvitrgle ivrrdwseia ketqarvlet ilkhgdveea
vrivkeviqk lanyeippe laiyeqitp lheykaighp vavaklaak gvkikpgmvi gyivlrgdgp isnrailae
ydpkhhkyda eyyienqvlp avlrilegfg yrkedlryqk trqvgltswl nikks (SEQ ID NO. 89)

> JDF-3 Thermococcus sp.

mildvdyitengkpvirvfk kengefrie ydrefepfyf allrddsaieeikkitaerhgrvkvkraekvkkkflgrsvevwlyfthp
qdvpairedkirkhpavidiyeydipfakry lidkglipme geeelklmsf dietlyhege efgtgpmilisyadesearvitwkkidlpv
vevvstekemikrflrvvkekdpdv lityn gdnfd faylkkrcelgvsf lgrdgsepki qrmgdrfavevkgvrhfdlypvirrtinl
ptytleavveavfgkpkkev yaeeiatawetgeglervarysmedarvtyelgreffpme aqlsrligqglwdvsrsstgnlvewflrk
ayernelapnkpderelarrggyaggyvkeperglwdnivyldfrslypsiiithnvspdtlnregcrsydvapevghkfckdfpgfip
sllgnlleerqkikrkmkatldpleknlldyrqaikilansyygygygyararwycrecaesvtawgre yiemvireleekfgfkvlyadt
dglhatipgadaetvkkkameflnyinpkpgleleyegfyvrgffv tkkkyavideegkitrgle ivrrdwseia ketqarvleailrh
gdveeavrivrevteklskyevppek lviheqitrelkdykatgphvaiaakraargv kirpgtvisyivlkgsgrigdraipdfedptkh
kydadyyienqvlpaverilrafgyrkedlryqktrqvglgawlkpkgkkk (SEQ ID NO. 90)

ACCESSION Q56366 9degN THERMOCOCCUS SP. (STRAIN 9°N-7).

mildtdyite ngkpvirvfk kengefkiey drtfepyfya llkddsaied vkkvtakrhg tvvkvkraek vqkkflgrpi evwklyfnhp qdvpairdri rahpavvdiy eydipfakry lidkglipme gdeeltmlaf dietlyhege efgtgpilmi syadgsearv itwkkidlpv vdvstekem ikrflrvvre kdpdvlityn gdnfdafaylk krceelgikf tlgrdgsepk iqrmgdrfav evkgrihfdl ypvirrtinl ptytleavye avfgpkpekv yaeiaqawe sgeglervar ysmedakvty elgreffpme aqlsrligqs lwdvsrsstg nlvewflrk aykrnelapn kpderelarr rggyaggyvk eperglwdni vyldfrslyp siiithnvsp dtlnregcke ydvapevghk fckdfpgfip slldlleer qkikrkmkat vdplekkllld yrqraikila nsfygyygya karwyckeca esvtawgrey iemvirelee kfgfkvlyad tdglhatipg adaetvkkka keflkyinpk lpglleleye gfyvrgffvt kkkyavidee gkittrglei vrrdwseiak etqarvleai lkhgdveeav rivkevtekl skyevppekl viheqitrdl rdykatgphv avakrlaarg vkirpgtvis yivlkgsgri gdraipadef dptkhrydae yyienqvlpa verilkafty rkedlryqkt kqvglgawlk vkgkk (SEQ ID NO. 91)

ACCESSION BAA06142 KOD *Pyrococcus* sp.

mildtdyite dgkpvirifk kengefkiey drtfepyfya llkddsaiee vkkitaerhg tvvtvkrvek vqkkflgrpv evwklyfthp qdvpairdki rehpaividiy eydipfakry lidkglvpme gdeelkmlaf dietlyhege efaegpilmi syadeegarv itwknvdlpv vdvsterem ikrflrvvke kdpdvlityn gdnfdafaylk krceklginf algrdgsepk iqrmgdrfav evkgrihfdl ypvirrtinl ptytleavye avfgqppekv yaeittawe tgenlervar ysmedakvty elgkeflpme aqlsrligqs lwdvsrsstg nlvewflrk ayernelapn kpdekelarr rqsyeggyvk eperglweni vyldfrchpa dtkvvvkgkg iinisevqeg dyvlgidgwq rvrkvweydy kgelvningl kctpnhklpv vtnerqtri rdsleksft kkvkkgiitt plfyegrat senipeeevl kgelagilla egtllrkdv yfdssrkkrr ishqyrveit igkdeeevfrd rityiferlf gitpsisekk gtnavtlkva kknvylkvke imdnieslha psvlrgffeg dgsvnrhrs ivatqgtkne wkiklvskll sqlgiphqty tyqqengkd rsryileitg kdglilfqt l igfiserkna llnkaisqre mnnlenngfy rlsefnvste yyegkyvdl legtpyyfan gilhnslyp siiithnvsp dtlnregcke ydvapqvghr fckdfpgfip slldlleer qkikkkmkat idpierklld yrqraikila nsilpeewlp vleegevhfv rigelidrmn eenagkvkre getevlevsg levpsfnrrt nkaelkrvka lirdysgkv ytirksgr r ikitsghslf svrngelnev tgdelkpgdl vavprrelp ernhvlnlve llltpeeet ldivmtipvk gkknffkgml rtlrwifgee krprtarryl rhledlgyvr lkkigyevld wdslnknyrrl yealvenvry ngnkreylve fnsirdavgi mplkelkewk igtlingfmr klievdesla klgyyvseg yarkqmpkn gwsysvklyn edpevlldme rlasrffgkv rrgmyveip kkigyllfen mcgvlaenkr ipefvftspk gvrlafleg yfigdgdvhp krllrstkse llanqlvll nsvgvsavkl ghdsqvyrvy ineelpfvkl dkkknayysh vipkevlsev fgkvfqknvs pqtfrkmved grldpekaqr lswliegdvv ldrvesvdve dydgyvydls vednenflvg fglvyahnsy ygygyarar wyckecaesv tawgreyitm tikeieekyg fkiysdtdg ffatipgada etvkkkamef lkyinaklpg aleleyegfy krgffvtkkk yavideegki ttrgleivrr dwseiaketq arveallkd gdvekavriv kevteklsky evppeklvih eqitrdldy katgphvava krlaargvki rpgtvisyiv lkgsgrigdr aipfdefdpt khkydaeyyi enqvlpaver ilrafgyrke dlryqktrqv glsawlkpkg t (SEQ ID NO. 92)

ACCESSION 4699806 Tgo *Thermococcus gorgonarius*.

mildtdyite dgkpvirifk kengefkidy drnfepiya llkddsaied vkkitaerhg ttvrvvraek vkkkflgrpi evwklyfthp qdvpairdki kehpavvdiy eydipfakry lidkglipme gdeelkmlaf dietlyhege efaegpilmi syadeegarv itwknidlpv vdvstekem ikrflkvvke kdpdvlityn gdnfdafaylk krseklgvkf ilgregsepk iqrmgdrfav evkgrihfdl ypvirrtinl ptytleavye aifgqppekv yaeiaqawe tgeglervar ysmedakvty elgkeffpme aqlsrlvgqs lwdvsrsstg nlvewflrk ayernelapn kpderelarr resyaggyvk eperglweni vyldfrslyp siiithnvsp dtlnregcee ydvapqvghk fckdfpgfip slldlleer qkvkkmkat idpiekkllld

yrqraikila nsfygyygya karwyckeca esvtawgrqy iettireiee kfgfkvlyad tdgffatipg adaetvkkka
kefldyina kpglleleye gfykrffvt kkkyavidee dkittgrlei vrrdwseiak etqarvleai lkhgdveeav
rivkevtekl skyevppekl viyeqitrdl kdykatgphv avakrlaarg ikirpgtvis yivlkgsgri gdraipfdef
dpakhkydae yyienqvlpa verilrafgy rkedlryqkt rqvlgawlk pkt (SEQ ID NO. 93)

ACCESSION P74918 THEFM *Thermococcus fumicolans*

mildtdyite dgrpvirvf kengefkies drdfepiya llkddsaied vkkitasrhg ttvrvragk vkkkflgrpi
evwklyfthp qdvpairedi rehpavvdi eydipfakry lidkglipme gdeelkmalf dietlyhege efaegpilmi
syadeegarv itwkkidpy vdvstekem ikrfkvvke kdpdvlityn gdnfdafaylk krseklgvkf ilgrdgsepk
iqrmgdrfav evkgrihfdl ypvirhtinl ptytleavye aifgqpkkev yaeeiaqawe tgeglervar ysmedakvty
elgreffpme aqlsrlvgqs fwdvsrsstg nlvewyllrk ayernelapn kpsgreterr rggyaggyvk eperglweni
ayldfrchpa dtkvivkgkg vvnisevreg dyvlgidgwq kvqrvweydy egelvningl kctpnhklpv vrterqtai
rdslaksflt kkvkglitt plfekigkie redvpeeeil kgelagiila egtllrkdv yfssrgkkr vshqyrveit
vgaqeedfqr rivyiferlf gvtpsvyrkk ntnaitfkva kkevylrvre imdgienlha psvlrgffeg dgsvnkvrkt
vvvnqgtne wkievvskll nklgiphrry tydyterekt mtthileiag rdglilfqi vgfisteknm aleearnre
vnrlennafy tladftakte yykgkvydlt legtpyyfan gilthnslyp siiishnvsp dtlnregcge ydeapqvghr
fckdfpgfip slldllder qkvkhhmkat vdpiekkld yrqraikila nsfygyygya karwyckeca esvtawgrqy
iettmreiee kfgfkvlyad svtgdtevti rmgriefvp ieklfervdh rvgekeycvl ggvealtldn rgrlvwkkvp
yvmrhktdkr iyrvwtfnsw yldvtedhsl igylntskvk pgkplkerlv evkpeelggk vkslitpnrp iartikanpi
avklweligl lvgdgnwggq snwakyyvgl scglkdaeie rkvlnporea svisnyydkk kkgdvsilsk wlagfmvkyf
kdengnkaip sfmfnlprey ieafnrlfs adgtvslrrg ipeirltsvn relsdavrkl lwlvgvsnsf ftetkpnryl ekesgthsih
vriknkhrfa drigflidr stklenslgg htnkkrayky dfdlvyrki eeitydgyvy dievegthrf fangilvhnt
dgffatipga daetvkkkar eflnyinplk pglleleyeg fyrrgffvt kkyavidee dkittgrlei rrdwsevae
tqarvleail rhgdveeavr ivkevtekl kyevppeklv iheqitrelk dykatgphva iakrlaargi kvrpgtvisy
ivlkgsgrig drtipfdefd ptkhrydae yienqvlpav erikafgyk kedlryqkt qvlgawlk gkk (SEQ ID
NO. 94)

ACCESSION O27276 METTH *Methanobacterium thermoautotrophicum*

medyrmvllid idyvtvdevp virfkgdks ggnepiahd rsfrpyiai ptdldeclre leelelekle vkemrdlgrp
teviriefrih pqdvpkirdr irdlesvrdi rehdiptyr ylidksivpm eeefqgvev dsapsvttvd rtvevtgrvq
stgsgahgld ilsfdievrn phgmpdpek dvmigvagn mgyesvista gdhldfvevv ederellerf aeividkkpd
ilvgynsdfn dfpyitrra ilgaeldlgw dgskirtmrr gfanataikg tvhvdlypvm rrymndryt lervyqelfg
eekidlpgrd lweywdrdel rdelfrysld dvvathriae kilplnelt rlvqqplfdi smatgqqae wflvrkayqy
gelvpnkpsq sdfssrrgr avgyvkepe kglhenivqf dfrslypsii iskniptdl tdeesecyv apegyrfrk
sprgfvpsvi geilservri keemkgsddp merkilnvqq ealkrlantm ygvygysrfr wysmecaeai tawgrdyikk
tiktaefgf htvyadtdgf yatyr (SEQ ID NO. 95)

ACCESSION Q58295 Metja

Methanococcus jannaschii

mgmsmgkiki dalidntykt iedkaviyly linsilkdrd fkyfyvelh kekvenedie kikeflknd llkfveniev
vkkilrkek evikiiathp qkvplrkik eceivkeiye hdpfakryl idneiipmty wdfenkkpvs ieipklksva
fdmevynrdt epnperdpil masfwdengg kvitykefnh pnievvknek elikkietl keydviytyn gdnfdpylk
arakiygidi nlkgdgeelk ikrggmeyrs yipgrvhidl ypisrllkl tkytledvvy nlfgieklki phtkivdywa
nndktlieys lqdakiytyki gkyffplevm fsrivrntpf eitrmssgqm veyllmkraf kenmivpnkp deeevrrrvl
tlyeggyvke pekgmfedii smdfchpkg tkvvvkgkgi vniedvkegn yvlgidgwqk vkkvwkyeye gelinvnglk
ctpnhkiplr ykikhkkink ndylvrdiya ksltkfkge gklilckdfe tignyekyin dmdedfilks eligillaeg
hlrrdieyf dssrgkkris hqyrveitvn edekdfieki kyifkklfny elyvrrkkgt kaitlgcakk diylkieeil
knkekylpna ilrgffegdg yvntvrravv vnqgtynydk ikfiaslldr lgikysfyty syeergkklk ryvieifskg
dlikfsilis fisrrknll neirqktly kigdygydl ddvcslesy kgevydltle grpyyfangi lthnslypsi iisynispdt
ldceckdvs ekilghwfck kkeglipktl nlierrini krmkkmaei geineeynll dyeqskkil ansilpdeyl
tiieedgikv vkigeyiddl mrkhkdkikf sgiseiletk nlktsfddki tkkceikkvk alirhpyfgk aykiklrsg
tikvtrghsl fkyengkive vkgddvrfgd livvpkkltc vdkevinip krlinadeee ikdlvitkhk dkaffvklk
tlediennkl kvifddcily lkelglidyn iikkinkvdi kildeekfka ykkyfdtvie hgnfkkgren iqyikikdyi
anipdkedef ceigaysgki nallkldekl akflgffvtr grlkkqklkg etvyeisvyk slpeyqkeia etfkevfag
smvkdktmd nkivylvlky ifkcgdkdkk hipeelflas esviksfldg flkakknshk gtstfmakde klynqlmilf
nlvgiptrft pvknkgykl lnpkygtvkd lmldevkeie afeysgyvyd lsvednenfl vnniyahnsy ygylafprar
fysrecaeiv tylgrkyile tvkeakfgf kvlyidtdgf yaiwkekisk eelikkamef veyinsklpg tmelefegyf
krgifvtkkr yalidengrv tvkglefvr dwsniakitq rrvleallve gsiekakkii qdvikdlrek kikkedliiy
tqltkdkey ktaphveia kklmregkri kvgdiigyii vkgtksiser aklpeevdid didvnyyidn qilppvlrim
eavgvsknel kkegaqltd kffk (SEQ ID NO. 96)

ACCESSION B56277 POC Pyrodictium occultum

mtetiefvll dssyeilgke pvvilwgiti dgkrvllldh rfrpyfyali argyedmvee iaasirrlsv vkspiidakp
ldkryfgrpr kavkittmip esvrhyreav kkiegvedsl eadifamry lidkrlypft vyripvedag mngfvrdrv
ykvagdpepl aditridlpp mrlvafdiev ysrrgsnpa rdpviivslr dsegkerlie aeghddrrvl refveyvraf
dpdiivgyns nhfdwpylme rarrlgikld vtrrvgaapt tsvyghvsq grlnvdlydy aeempeikmk tleevaeylg
vmkkservii ewwripeywd dekkqllr yalddvraty glaekmlpfa iqlstvtgvp ldqvgamvgv frlewylmra
aydmnelvpv rverrgesyk gavvlkplkg vhenvvldf ssmypsimik ynvdpdtivd dpsecpygg cyvapevghr
frrppgffk tvlenllkl rqvkekmlkef ppspeyrly derqkalkvl anasygymgw sharwyckrc aeavtawgrn
liltaieyar klgkviygd tdsfivvydk ekvekliefv ekelgfeiki dkiykvfft eakkryvgll edgridivgf
eavrgdwcel akevqekaee ivlntgnvdk aisirevik qlregkvpit kliiwktlsk rieeyehdap hvmaarmke
agyevspgdk vgyvivkgsg svssraypyf mvdpstidvn yyidhqivpa alrilsyfgv tekqlkaaat vqrslfdffa skk
(SEQ ID NO. 97)

ACCESSION BAA81109 ApEI Aeropyrum pernix

mrgstpvii wrggadgsrv vvygefrpy fyvlpdgsdg ldqlaamirr lsrpsspils vervrrfig revealkvtt
lvpasvreyr eavrrlgvr dvleadipfa lrfidfnly pmrwyvaevr evavphgysv draytllsgdi redetriqed
plglrvmaf dievyskmrt pdpkdpvim iglqqaggei eileaersd kkviagfver vksidpdviv gynqrfdwp
ylverarvlv vklavgrsv epqglyghy svsglnvdl ldfaelhev kvktleevad ylgvvkiger vtlewqqige
ywddpskrei lrkylrddvr stmglaekfl pfgaelsqvs glpddqmaa svgrlewrl ireaaklgel vprnverseg

ryagaivlrp kpgvhediav ldfasmypni mvkynvgpdt lvrpgeeyge eevytapevg hkfrksppgf fkkilerfls
wrrqirsemk khppdspeyk llderqkaik llanasygym gwpharwycr ecaeavtawg rsiirtairk agelgleviy
gdttdslfvkn dpekverlir fveelgfdi kvdkvyrrvf fteakkryvg ltvdgkidvv gfeavrgdws elaketqfkv
aeivlktgsv deavdyvni ieklrrgqvd mrklviwktl trppsmyear qphvtaallm eragikvepg akigyvvtkg
sgplytrakp yfmaskeevd veyyvdkqv paalrilqyf gvtekrkkg grqstlldfm rrkg (SEQ ID NO. 98)

ACCESSION O29753 ARCFU Archaeoglobus fulgidus

mervegwlid adyetiggka vvrlwckddq gifvaydynf dpyfyvigvd edilknaats trrevikls fekaqlktlg
reveyyivya hhpqhvpklr dylsqfgdvr eadipfayry lidkdacmd giaiegekqg gvirsykiek veriprmeff
elkmlvfdce mlssfgmpep ekdpiiivsv ktndddeiil tgderkiisd fvkliksydp diivgynqda fdwpylrkra
erwnipldvg rdgsnvvfgr grpkitgrln vdlydiamri sdikikklen vaeflgtkie iadieakdiy rywsrgekek
vlnyarqda ntyliakell pmhyelskmi rlpvddvtrm grgqvdlwll lseakkigei apnppehaes yegafvlepe
rglhenvacl dfasmypsim iafnispdty gcrddcyep evghkfrksp dgffkrilm liekrrelkv elknspess
eyklldikqq tlkvlnsfy gymgwnlarw ychpcaeatt awgrhfirts akiaesmgfk vlygtdtsif vtkagmtked
vdrldklhe elpiqievde yysaiffvek kryagltedg rlvvkglevr rgdwcelakk vqrevievil keknpekals
lvkdvilrik egkvsleevv iykgltkps kyesmqahvk aalkarengi iypvsskigy vivkgsngn draypidlie
dfdgenlrik tksgieikkl dkdyidnqi ipsvrliler fgyteaslk ssqmsldsff s (SEQ ID NO. 99)

ACCESSION 6435708 Desulfurococcus sp. Tok.

mildadyite dgkpvirvfk kekgefkiy drdfepyia llkddsaied ikkitaerhg ttvrvtraer vkkkflgrpv
evwklyfthp qdvpairdki rehpaavdiy eydipfakry lidrglipme gdeelmlaf dietlyhege efgegpilmi
syadeegarv itwknidpy vesvstekem ikrflkviqe kdpdvlityn gdnfdfaylk krsemlgvkf ilgrdgsepk
iqrmgdrfav evkgrihfdl ypvirrtinl ptytleavye pvfgpkpek vyaeeiarawe sgeglervar ysmedakaty
elgkeffpme aqlsrlvgqs lwdvsrsstg nlvewflrk ayernvapn kpderelarr tesyaggyvk epeklweni
vyldykslyp siiithnvsp dtlnregcre ydvapqvghr fckdfpgfip slgdlleer qkvkkmkat vdpierklld
yrqraikila nsyygyyaya narwycreca esvtawgrqy iettmreiee kfgfkvlyad tdgffatipg adaetvknka
keflnyinpr lpglleeye gfyrrgffvt kkkyavidee dkittglei vrrdwseiak etqarvleai lkhgdveeav
rivkevtekl srhevppekl viyeqitrdl rsyratgphv avakrlaarg ikirpgtvis yivlkgpgrv gdraipfdef
dpakhrydae yyienqvlpa verilrafgy rkedlryqkt kqaglgawlk pkt (SEQ ID NO. 100)

ACCESSION Q56366 9oN-7

mildtdyite ngkpvirvfk kengefkley drtfepyfya llkddsaied vkkvtakrhg tvvkvkraek vqkkflgrpi
evwklyfnhp qdvpairdri rahpaavdiy eydipfakry lidkglipme gdeeltmlaf dietlyhege efgtgpilmi
syadgsearv itwkkidpy vdvstekem ikrflrvre kdpdvlityn gdnfdfaylk krceelgikf tlgrdgsepk
iqrmgdrfav evkgrihfdl ypvirrtinl ptytleavye avfgpkpek vyaeeiaqawe sgeglervar ysmedakvty
elgreffpme aqlsrligqs lwdvsrsstg nlvewflrk ayknelapn kpderelarr rggyaggyvk eperglwdni
vyldfrslyp siiithnvsp dtlnregcke ydvapevghk fckdfpgfip slgdlleer qkikrkmkat vdplekkld
yrqraikila nsfygygya karwyckeca esvtawgrey iemvirelee kfgfkvlyad tdglhatipg adaetvkkka
keflkyinpk lpglleeye gfyvrgffvt kkkyavidee gkittglei vrrdwseiak etqarvleai lkhgdveeav

rivkevtekl skyevppekl viheqitrld rdykatgphv avakrlaarg vkirpgtvis yivlkgsgri gdraipadef
dptkhrydae yyienqvlpa verilkafty rkedlryqkt kqvglgawlk vkgkk (SEQ ID NO. 101)

ACCESSION O29753 Afu

mervegwlid adyetiggka vvrlwckddq gifvaydynf dpyfyvigvd edilknaats trreviklks fekaqlktlg
revegyivya hhpqhvpklr dylsqfgdvr eadipfayry lidkdacmd giaiegekqg gvirsykiek veriprmeff
elkmlvfdce mlssfgmpep ekdpiiivsv ktndddeiil tgderkiisd fvkliksydp diivgynqda fdwpylrkra
erwnipldvg rdgsnvvfrg grpkitgrln vdlydiamri sdikikklen vaeflgtkie iadieakdiy rywsrgekek
vlnyarqdai ntyliakell pmhyelskmi rlpvddvtrm grgkqvdlwll lseakkigei apnppehaes yegafvlepe
rglhenvacl dfasmypsim iafnispdty gcrddcyeap evghkfrksp dgffkrilrm liekrrelkv elknspess
eyklldikqq tlkvltnsfy gymgwnlarw ychpcaeatt awgrhfirts akiaesmgfk vlygdtdsif vtkagmtked
vdrldiklke elpiqievde yysaiffvek kryagltedg rlvvkglevr rgdwcelakk vqrevievil keknpekals
lvkdvilrik egkvsleevv iykgltkps kyesmqahvk aalkaremgi iypvsskigy vivkgsgnig draypidlie
dfdgenlrik tksgieikkl dkdyidnqi ipsvrlirer fgyteaslk ssqmsldsff s (SEQ ID NO. 102)

ACCESSION P52025 Mvo

mdldynskdl cidmyykneg lkkpeinlqk ecefkpyfyv dtsepkeiyd yldglnqeid lkklepafen ntslkvqdli
tnieiekiv ysdylngkd isevsdfknk kerkickvyv kypnhvkiir eyfkefgksy efdipflrry midqdivpsa
kysednkidn sipelnciaf dmelyckkep nakkdpiimv nlskdyyqv itykkfense yngcvdyvkd ekeliqkie
ilkqydivyt yngdnfdpy lkkraniei eldfdnasns qqpqiikisk gginrkskip giihidlypi arklnlntky
klenvvqelf kinkeavdyg dipkmweted tllryayed alytykmgny flpleimfsr invqplydts rmnssqmvef
lllksfeqn mispnrpsss syrerakfsy eggyvreplk giqedivslid fmslypsili shnispetvi yeekerenme
lgiipktlne llsrrkhikm llkdkiqkne fdeysrleh eqksikvlan shygylafpm arwysdkcae mvtglrkyi
qetiekaef gfkviyaddt gfyakwdydk lqkgkkeend ksdkslnlpk lskeeliilt kkflkginee lpegmelefe
ghfkrglftv kkkyaliedd ghivvkglev vrrdwsniak dtqqaviral ledgdvnlak kiiktndnl kkgnidkndl
lihtqltkni eeykstaphi evakkikqrg dsrvrgdvis yivvgsrsi seraellaya gdydinyid nqvlppviri
meslgisede lknsgkqfkl dqfm (SEQ ID NO. 103)

ACCESSION AAF27815

melkvwpldi tyavvgvspe irifgilssg ervvlidrsf kpyfyvdcav cepaalktal srvapiddvq iverflgrs
kkflkviaki pedvrklrea amsiprvsgv yeadirfymr ymidmgvvpw swnvaeveeg grlgiptyv vsqwygideg
fppslkvmaf dievynersg pdpirdpvm laiktndghe evfeasgkdd rgvvrafvdf irsydpdviv gysngfdwp
ylverakavg vplkvdrln ppqqsvyghw sivgranvdl yniveefpei klktldrvae yfgvmkreer vlipghkiye
ywkdpnkrpl lkryvlddv stlgldkll pfliqlssvs glpldqvaas svgnrvewml lryayrlgev apnreereye
pykgavlepe kpgmyedvlv ldfssmyni mmkynlspdt ylepegdpp egvnvapevg hrfrsppgf vpqvlkslve
lrkavreeak kyppdspefk ilderqralk vmanaiygyl gwvgarwykr evaesvtafa railkdvieq arlgivvvy
gdtdslfvkk hgdvdikly veekygidik vdkdyakvlf teakkryagl lrdgridvg fevvrgdwse lakdvqlrvi
eiilksrdv earhgvikiy reierlkny kfniddliw ktldkeldey kaypphvhhaa qilkrhgyrv gkggtigyvi
vkggekvser alpyillddi kkididyie rqiipaali aevigvkesd lktgrmersl ldfls (SEQ ID NO. 104)

ACCESSION AAC62712 Csy

mtvqdaveip psllvsatyed sqagavvlkf yepesqkivh wtdntghkpy cytrqppsel gelegredvl gteqvmrhdli
iadkdvpvtk itvadplaig gtnseksirn imdtwesdik yyenlydks lvvgyrysvs ggkviphdmp isdevklalk
sllwdkvvde gmadrkefre fiagwadlln qpiprirrls fdievdseeg ripdpkisdr rvtavgfaat dglkqvfvlr
sgaeegengv tpgvevvfyd keadmirdal svigsypfvl tyngddfdmp ymlnrarrlg vsdsdiplym mrdsatlrhg
vhldlyrtfs nrsfqlyafa akytdyslms vtkamlgegk vdygvklgdl tlyqtanycy hdarltlels tfgneilmld
lvvtsriarm piddmsrmgv sqwirsllyy ehrqmalip rrdelegrsr evsndavikd kkfrgglvve peegihfdvt
vmdfaslyps iikvrnlsye tvrcvhaeck kntipdtnhw vctknnglts miigslrdlr vnnykslsks tsiteeqrqq
ytvisqalkv vlnasygvmg aeifplyflp aaeattavgr yiimqtishc eqmgvrvlyg dtdslfikdp eerqiheive
hakkehgvcl evdkeyryvv lsnrkknfyg vtragkvdkv gltgkkshtp pfikelfysl ldilsgvese defesakmri
skaiaacgr leerqiplvd lafnvmiska pseyvktvpq hiraarllen arevkkgdii syvkvmmktg vkpvmemarag
evdtskylef mestldqlts smglfdfeil gkpkqtgmeq fffk (SEQ ID NO. 105)

ACCESSION P95690 Sac

mskqatlfdf sikkneskeq tnqesvevpk qtanrtkiew ikeaedgkvy flqvdvdgk ksravcklyd kegkkiyimq
desghkpyfl tddidpdkvnl itkvvrpsf dhlelinkvd pytgkkirtl kivvkdplav rrmrsslpa yeahikyynn
yvydnglipg liyvknkgkl tqlnpelkge eineikklsd ayemtketvn dwipiletev pdikrvsldi evytpnrgri
pdperaeffi isvalagndg skivlalkre dvnsdfskkd gvqveifdse kllarlfei ireypmlltf ngddfdipyi
yfralrlnfs peevpldvvs gegkflagih idlykfffnr avsiyafegk yseyslyava tallgiskvk ldtfifmndi
dklieynlrd aeitlklttf nnnlvklmv llarisklgl eeltrtevt wiknlyyweh rkwnwliplk eelvrnsqv
ktaavikgkk ykgavvidpp agvyfnvvvl dfaalspsi knwnisyeti eidectkkvw vedetgeklh yvcmdkpgit
avyqglirdf rvkvvykkak ysniseeqrs lydvvqramk vfinatygvf gaenfpalya avaesvtaig ryiitttykq
aeklnlkviy gtdslflyn ptkdkleeli kfvdqfnld levndtykyv aysglkknyf gvypdgktei kgmlakkmt
pifikkefae iknmlaslms pndipevknk leikikdiyy klnkgynd dlafrimlsk pldsytntp qhvkgqlr
afgvnlprd vimfvkvksk dgvkayqlak iseidiekv etlrttfeqi lkafgiswde ivstisidsf fgskk (SEQ ID
NO. 106)

ACCESSION BAA23994 Soh

marqitlfdf tlkkeqnkde srkeephan ineerrkpe wikeaegks yllqvdydg kkskaickly dketkkiyil
ydnthkpyf ltdidpekn kipkvvrps fdhletviki dpysgnkikl tkivvkdpla vrmrnsvpk ayeahikyfn
nyiylglip glpyvvkkgk leqlpelkg eevdeirkaf adsdemptea vndwipifes evpdvkrvai dievytpikg
ripdekaef piisislagn dgtrvllv redvnsqitk hdvivetfks erelirffd iildypiilt fngddfdipy iyralklnf
tpeepfdii ndegkylagi hidlykfffn raimyafeg kyneynldav atallgmskv kldtlisfld ldklieynsr daeitlkltt
fnnlvwklil illariskmg leeltrtevs twiknlywe hrrnwlipl keeiltrssq iktaaiikgk rykgavvidp
pagvffnvvv ldfaslypsi imwnisyet vdvencnke yvrdetgevl hyickdkpgi tavitglld frkvvykkka
ksqniseeqr svydvqram kvfinatygv fgaenfpalya pavaesvtai gryvittvn ycsigllqv ygtdsmflw
npskekleeli ikfvkgkfgl dlevdkvykf vafsglkkny lgypdgktd ikgmllakkn tpefikkefn evkqlvttn
spddipkird qleykikeiy eklrhkgynl delafrvmls kplesytnt pghvkaalql rsygvmlpr diimfvkvks
kdgvkpvqla klseidvdky idavrstfeq ilkafgliga nllqlsils lt (SEQ ID NO. 107)

ACCESSION P26811 Sso

mtkqltlfdi psskpakseq ntqqsqqsap veekkvvrre wleeaqenki yflqvydydg kkgkavcklf dketqkiyal
ydntghkpyf lvdlepdkvg kipkivrdps fdhietvski dpytwnkfkl tkivvrdpla vrrlmdvpk ayeahikyfn
nymydiglip gmpyvvnkgk lesvylslde kdveeikkaf adsdemtrqm avdwlpiwet eipkikrvai dievytpvkg
ripdsqkaef piisialags dglkkvvlvln rmdvnegsvk ldgisverfn teyellgrff dilleypivl tfngddfdlp yiyfralkg
yfpeeipidv agkdeakyla glhidlykff fnkavrnyaf egkyneynld avakallgts kvkvdtlisl ldveklieyn
frdaeitql ttfndltmk livlfsrisr lgieeltrte istwvknlyy wehrkwnli plkeeilaks snirtsalik gkykgavvi
dppagiffni tvldfaslyp siirtwnlsy etvdiqqckk pyevkdetge vlhivcmdrp gitavitgll rfrvkiykk
kaknpnnsee qkllydvvr amkvfinaty gvfgaetfpl yapavaesvt algryvitst vkkareegt vlygtdslf
llnppknsle niikwvkttf nldlevdkty kfvaefglkk nyfgvyqdgk vdikgmlvkk rntpefvkkv fnevelmis
inspndvkei krkivdvvg syeklknkgy nldelafkvm lskpldaykk ntpqhvaal qlrpfgvnl prdiyyvkv
rskdgvkpvq lakvteidae kylealrstf eqilrafgvs wdeiaatmsi dsffsypskg ns (SEQ ID NO. 108)

Please note that only upper-case letters are considered to be aligned.

Figure 7B

Alignment (DIALIGN format):

Pfu	1	MILDVDYITE	EGKPVIRLFK	KENGKFKIEH	DRTFRPYIYA	LLRDDSKIEE
Tgo	1	MILDTDYITE	DGKPVIRIFK	KENGFEKIDY	DRNFEPYIYA	LLKDDSAIED
KOD	1	MILDTDYITE	DGKPVIRIFK	KENGFEKIEY	DRTFEPYFYA	LLKDDSAIEE
Vent	1	MILDTDYITK	DGKPIIRIFK	KENGFEKIEL	DPHFQPYIYA	LLKDDSAIEE
Deep	1	MILDADYITE	DGKPIIRIFK	KENGFEKVEY	DRNFRPYIYA	LLKDDSQIDE
JDF-3	1	MILDVDYITE	NGKPVIRVFK	KENGFEFRIEY	DREFEPYFYA	LLRDDSAIEE

V93

Pfu	51	VKKITGERHG	KIVRIVDVEK	VEKKFLGKPI	TVWKLYLEHP	QDVPTIREKV
Tgo	51	VKKITAERHG	TTVRVVRAEK	VKKKFLGRPI	EVWKLYFTHP	QDVPAIRDKI
KOD	51	VKKITAERHG	TVVTVKRVEK	VQKKFLGRPV	EVWKLYFTHP	QDVPAIRDKI
Vent	51	IKAIKGERHG	KTVRVLDVAVK	VRKKFLGREV	EVWKLIFEHP	QDVPAMRGKI
Deep	51	VRKITAERHG	KIVRIIDAOK	VRKKFLGRPI	EVWRLYFEHP	QDVPAIRDKI
JDF-3	51	IKKITAERHG	RVVKVKRAEK	VKKKFLGRSV	EVWVLYFTHP	QDVPAIRDKI

DXE (exo I)

Pfu	101	REHPAVVDIF	EYDIPFAKRY	LIDKGLIPME	GEEELKILAF	DIETLYHEGE
Tgo	101	KEHPAVVDIY	EYDIPFAKRY	LIDKGLIPME	GDEELKMLAF	DIETLYHEGE
KOD	101	REHGAVIDIY	EYDIPFAKRY	LIDKGLVPM	GDEELKMLAF	DIQTLYHEGE
Vent	101	REHPAVVDIY	EYDIPFAKRY	LIDKGLIPME	GDEELKLLAF	DIETLYHEGD
Deep	101	REHSAVIDIF	EYDIPFAKRY	LIDKGLIPME	GDEELKLLAF	DIETLYHEGE
JDF-3	101	RKHPAVIDIY	EYDIPFAKRY	LIDKGLIPME	GEEELKLMSE	DIETLYHEGE

111 121 131 141-143

Pfu	151	EFGKGPIIMI	SYADENEAKV	ITWKNIDLPI	VEVSSSEREM	IKRFLRIIRE
Tgo	151	EFAEGPILMI	SYADEEGARV	ITWKNIDLPI	VDVVSTEEKM	IKRFLKVVKE
KOD	151	EFAEGPILMI	SYADEEGARV	ITWKNVDLPI	VDVVSTEREM	IKRFLRVVKE
Vent	151	EFGKGEIIMI	SYADEEEARV	ITWKNIDLPI	VDVVSNEREM	IKRFVQVVKE
Deep	151	EFAKGPIIMI	SYADEEEAKV	ITWKKIDLPI	VEVSSSEREM	IKRFLKVIRE
JDF-3	151	EFGTGPILMI	SYADESEARV	ITWKKIDLPI	VEVVSTEEKM	IKRFLRVVKE

NX₂₃FD (exo II)

Pfu	201	KDPDIIVTYN	GDSFDLPYLA	KRAEKLGIKL	TIGRDGS—E	PKMQRIGDMT
Tgo	201	KDPDVLITYN	GNFDFAYLK	KRSEKLGKVF	ILGREGS—E	PKIQRMGDRF
KOD	201	KDPDVLITYN	GNFDFAYLK	KRCEKLGINF	ALGRDGS—E	PKIQRMGDRF
Vent	201	KDPDVIITYN	GNFDFLYLI	KRAEKLGVRL	VLGRDkehpe	PKIQRMGDSF
Deep	201	KDPDVIITYN	GDSFDLPYLV	KRAEKLGIKL	PLGRDGS—E	PKMQRLGDMT
JDF-3	201	KDPDVLITYN	GNFDFAYLK	KRCEKLGVSF	TLGRDGS—E	PKIQRMGDRF

210-215 231 239

Pfu	249	AVEVKGRIHF	DLYHVITRTI	NLPTYTLEAV	YEAIFGKPKE	KVYADEIAKA
Tgo	249	AVEVKGRIHF	DLYPVIRRTI	NLPTYTLEAV	YEAIFGQPKKE	KVYAEETPA
KOD	249	AVEVKGRIHF	DLYPVIRRTI	NLPTYTLEAV	YEAIFGQPKKE	KVYAEETPA



Vent	251	AVEIKGRIHF	DLFPVVRTI	NLPTYTLEAV	YEAVLGKTKS	KLGAEEIAAI
Deep	249	AVEIKGRIHF	DLYHVIRRTI	NLPTYTLEAV	YEAIFGKPK	KVYAHEIAEA
JDF-3	249	AVEVKG RVHF	DLYPVIRRTI	NLPTYTLEAV	YEA VFGKPK	KVYAEIATA

Y₃D (exo III)

Pfu	299	WESGENLERV	AKYSMEDAKA	TYELGKEFLP	MEIQLSRLVG	QPLWDVSRSS
Tgo	299	WETGEGLERV	ARYSMEDAKV	TYELGKEFFP	MEAQLSRLVG	QSLWDVSRSS
KOD	299	WETGENLERV	ARYSMEDAKV	TYELGKEFLP	MEAQLSRLIG	QSLWDVSRSS
Vent	301	WETEESMKKL	AQYSMEDARA	TYELGKEFFP	MEAEALAKLIG	QSVWDVSRSS
Deep	299	WETGKGLERV	AKYSMEDAKV	TYELGREFFP	MEAQLSRLVG	QPLWDVSRSS
JDF-3	299	WETGEGLERV	ARYSMEDARV	TYELGREFFP	MEAQLSRLIG	QGLWDVSRSS

311-315

Pfu	349	TGNLVEWFLL	RKAYERNEVA	PNKPSEEEYQ	RRLRESYTG	FVKEPEKGLW
Tgo	349	TGNLVEWFLL	RKAYERNELA	PNKPDERELA	RR-RESYAGG	YVKEPERGLW
KOD	349	TGNLVEWFLL	RKAYERNELA	PNKPDEKELA	RR-RQSYEGG	YVKEPERGLW
Vent	351	TGNLVEWYLL	RVAYARNELA	PNKPDEEEYK	RRLRTTYLGG	YVKEPEKGLW
Deep	349	TGNLVEWYLL	RKAYERNELA	PNKPDEREYE	RRLRESYAGG	YVKEPEKGLW
JDF-3	349	TGNLVEWFLL	RKAYERNELA	PNKPDERELA	RR-RggYAGG	YVKEPERGLW

Pfu	399	ENIVYLD FRA	LYPSIIITHN	VSPDTLNLEG	CKNYDIAPQV	GHKFCKDIPG
Tgo	398	ENIVYLD FRS	LYPSIIITHN	VSPDTLNREG	CEEYDVAPQV	GHKFCKDFPG
KOD	398	ENIVYLD FRS	LYPSIIITHN	VSPDTLNREG	CKEYDVAPQV	GHRFCKDFPG
Vent	401	ENIIYLD FRS	LYPSIIIVTHN	VSPDTLEKEG	CKNYDVAPIV	GYRFCKDFPG
Deep	399	EGLVSLD FRS	LYPSIIITHN	VSPDTLNREG	CREYDVAPEV	GHKFCKDFPG
JDF-3	398	DNIVYLD FRS	LYPSIIITHN	VSPDTLNREG	CRSYDVAPEV	GHKFCKDFPG

Pfu	449	FIPSLLG HLL	EERQKIKTKM	KETQDPIEKI	LLDYRQKAIK	LLANSFYGY
Tgo	448	FIPSLLG DDL	EERQKVKKKM	KATIDPIEKK	LLDYRQRAIK	ILANSFYGY
KOD	448	FIPSLLG DDL	EERQKIKKKM	KATIDPIERK	LLDYRQRAIK	ILANSFYGY
Vent	451	FIPSILG DLI	AMRQDIKKKM	KSTIDPIEKK	MLDYRQRAIK	LLANSFYGY
Deep	449	FIPSLLK RLL	DERQEIKRKM	KASKDPIEKK	MLDYRQRAIK	ILANSFYGY
JDF-3	448	FIPSLLG NLL	EERQKIKRKM	KATLDPLEKN	LLDYRQRAIK	ILANSFYGY

Pfu	499	GYAKARWYCK	ECAESVTAWG	RKYIELVWKE	LEEKFGFKVL	YIDTDGLYAT
Tgo	498	GYAKARWYCK	ECAESVTAWG	RQYIETTIRE	IEEKFGFKVL	YADTDGFFAT
KOD	498	GYARARWYCK	ECAESVTAWG	REYITMTIKE	IEEKYGFKVI	YSDTDGFFAT
Vent	501	GYPKARWYSK	ECAESVTAWG	RHYIEMTIRE	IEEKFGFKVL	YADTDGFFAT
Deep	499	GYAKARWYCK	ECAESVTAWG	REYIEFVRKE	LEEKFGFKVL	YIDTDGLYAT
JDF-3	498	GYARARWYCR	ECAESVTAWG	REYIEMVIRE	LEEKFGFKVL	YADTDGLHAT

Pfu	549	IPGGESEEEK	KKALEFVKYI	NSKLPGLLEL	EYEGFYKRGF	FVTKKRYAVI
Tgo	548	IPGADAETVK	KKAKEFLDYI	NAKLPGLLEL	EYEGFYKRGF	FVTKKRYAVI

KOD	548	IPGADAETVK	KKAMEFLNYI	NAKLPGALEL	EYEGFYKRGF	FVTKKKYAVI
Vent	551	IPGEKPELIK	KKAKEFLNYI	NSKLPGLLEL	EYEGFYLRGF	FVTKKRYAVI
Deep	549	IPGAKPEEIK	KKALEFVDYI	NAKLPGLEL	EYEGFYVRGF	FVTKKKYALI
JDF-3	548	IPGADAETVK	KKAMEFLNYI	NPKLPGLLEL	EYEGFYVRGF	FVTKKKYAVI

Pfu	599	DEEGKVITRG	LEIVRRDWE	IAKETQARVL	ETILKHGDVE	EAVRIVKEVI
Tgo	598	DEEDKITTRG	LEIVRRDWE	IAKETQARVL	EAILKHGDVE	EAVRIVKEVT
KOD	598	DEEGKITTRG	LEIVRRDWE	IAKETQARVL	EALLKGDGVE	KAVRIVKEVT
Vent	601	DEEGRITTRG	LEVRRDWE	IAKETQAKVL	EAILKEGSVE	KAVEVVRDVV
Deep	599	DEEGKIITRG	LEIVRRDWE	IAKETQAKVL	EAILKHGNVE	EAVKIVKEVT
JDF-3	598	DEEGKITTRG	LEIVRRDWE	IAKETQARVL	EAILRHGDVE	EAVRIVREVT

Pfu	649	QKLANYEIPP	EKLAIYEQIT	RPLHEYKAIG	PHVAVAKKLA	AKGVKIKPGM
Tgo	648	EKLSKYEVP	EKLVIYEQIT	RDLKDYKATG	PHVAVAKRLA	ARGIKIRPGT
KOD	648	EKLSKYEVP	EKLVIHEQIT	RDLKDYKATG	PHVAVAKRLA	ARGVKIRPGT
Vent	651	EKIAKYRVPL	EKLVIHEQIT	RDLKDYKAIG	PHVAIAKRLA	ARGIKVKPGT
Deep	649	EKLSKYEIPP	EKLVIYEQIT	RPLHEYKAIG	PHVAVAKRLA	ARGVKVRPGM
JDF-3	648	EKLSKYEVP	EKLVIHEQIT	RELKDYKATG	PHVAIAKRLA	ARGVKIRPGT

Pfu	699	VIGYIVLRGD	GPISNRAILA	EEYDPKKHKY	DAEYYIENQV	LPAVLRILEG
Tgo	698	VISYIVLKGS	GRIGDRAIPF	DEFDPAKHKY	DAEYYIENQV	LPAVERILRA
KOD	698	VISYIVLKGS	GRIGDRAIPF	DEFDPTKHKY	DAEYYIENQV	LPAVERILRA
Vent	701	IISYIVLKGS	GKISDRVILL	TEYDPRKHKY	DPDYIENQV	LPVLRILEA
Deep	699	VIGYIVLRGD	GPISKRAILA	EEFDLRKHKY	DAEYYIENQV	LPVLRILEA
JDF-3	698	VISYIVLKGS	GRIGDRAIPF	DEFDPTKHKY	DADYYIENQV	LPAVERILRA

Pfu	749	FGYRKEDLRY	QKTRQVGLTS	WLNKKs---
Tgo	748	FGYRKEDLRY	QKTRQVGLGA	WLKPKt---
KOD	748	FGYRKEDLRY	QKTRQVGLSA	WLKPKgt---
Vent	751	FGYRKEDLRY	QSSKQTGLDA	WLKt-----
Deep	749	FGYRKEDLRW	QKTKQTGLTA	WLNKKk---
JDF-3	748	FGYRKEDLRY	QKTRQVGLGA	WLKPKGkkk

Alignment (FASTA format):

```

>Pfu
MILDVDYITEEGKPVIRLFKKENGKFKIEHRTFRPYIYALLRDDSKIEE
VKKITGERHGKIVRIVDVEKVEKKFLGKPITVWKLYLEHPQDVPTIREKV
REHPAVVDIFEYDIPFAKRYLIDKGLIPMEGEEELKILAFDIETLYHEGE
EFGKGPIIMISYADENEAKVITWKNIDLPYVEVVSSSEREMIKRFLRIIRE
KDPDIIVTYNGDSFDFPYLAKRAEKLGIKLTIGRDGS--EPKMQRIGDMT
AVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKKEKVYADEIAKA

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WESGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSS
TGNLVEWFLLRKAYERNEVAPNKPSEEEYQRRRESYTGGFVKEPEKGLW
ENIVYLDLFRALYPSIIITHNVSPDTLNLEGCKNYDIAPQVGHKFKCDIPG
FIPSLGLHLEERQKIKTKMKETQDPIEKILLDYRQKAIKLLANSFYGY
GYAKARWYCKEACESVTAWGRKYIELVWKELEEKFGFKVLYIDTDGLYAT
IPGGESEEEKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVI
DEEGKVITRGLIIVRRDWSEIAKETQARVLETILKHGDVEEAVRIVKEVI
QKLANYEIPPEKLAIYEQITRPLHEYKAIGPHVAVAKLAAGVKIKPGM
VIGYIVLRGDPISNRAILAEYDPKKHKYDAEYYIENQVLPVLRILEG
FGYRKEDLRYQKTRQVGLTSWLNIKKs—

>Tgo

MILDTDYITEDGKPVIRIFKKENGFEFKIDYDRNFEPYIYALLKDDSAIED
VKKITAERHGTTVRVVRAEKVKKFLGRPIEVWKL YFTHPQDVPAIRDKI
KEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGE
EFAEGPILMISYADEEGARVITWKNIDL PYVDVSTEKEMIKRFLKVKE
KDPDVLITYNGDNDFAYLKKRSEKLGKVFILGREGS—EPKIQRMGDRF
AVEVKGRIFHDLYPVIRRTINLPTYTLEAVYEAIFGQPKKEKVYAEETIAQA
WETGEGLERVARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSS
TGNLVEWFLLRKAYERNELAPNKPDERELARR—RESYAGGYVKEPERGLW
ENIVYLDLFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFKCDFPG
FIPSLGLDLLEERQKVKKMKATIDPIEKLLDYRQRAIKILANSFYGY
GYAKARWYCKEACESVTAWGRQYIETTIREIEEKFGFKVLYADTDGFFAT
IPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKRYAVI
DEEDKITTRGLEIIVRRDWSEIAKETQARVLEAILKHGDVEEAVRIVKEVT
EKLSKYEVPPPEKLVIYEQITRDLKDYKATGPHVAVAKRLAARGIKIRPGT
VISYIVLKGSGRIGDRAIPFDEFDPKHKYDAEYYIENQVLP AVERILRA
FGYRKEDLRYQKTRQVGLCAWLKPKt—

>KOD

MILDTDYITEDGKPVIRIFKKENGFEFKIEYDRTFEPYFYALLKDDSAIEE
VKKITAERHGTTVTVKRVEKVQKKFLGRPVEVWKL YFTHPQDVPAIRDKI
REHGAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIQTLYHEGE
EFAEGPILMISYADEEGARVITWKNVDLPYVDVSTEREMIKRFLRVVKE
KDPDVLITYNGDNDFAYLKKRCEKLGINFALGRDGS—EPKIQRMGDRF
AVEVKGRIFHDLYPVIRRTINLPTYTLEAVYEAIFGQPKKEKVYAEETIPA
WETGENLERVARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSS
TGNLVEWFLLRKAYERNELAPNKPDEKELARR—RQSYEGGYVKEPERGLW
ENIVYLDLFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHKFKCDFPG
FIPSLGLDLLEERQKIKKKMKATIDPIERKLLDYRQRAIKILANSYGY
GYARARWYCKEACESVTAWGREYITMTIKEIEEKYGFVYISDTGFFAT
IPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKRYAVI
DEEGKITTRGLEIIVRRDWSEIAKETQARVLEALLKGDVKEAVRIVKEVT
EKLSKYEVPPPEKLVIHEQITRDLKDYKATGPHVAVAKRLAARGVKIRPGT
VISYIVLKGSGRIGDRAIPFDEFDPKHKYDAEYYIENQVLP AVERILRA
FGYRKEDLRYQKTRQVGLSAWLKPKGt—

>Vent

MILDTDYITKDGPPIIRIFKKENGFEKIELDPHFQPYIYALLKDDSAIEE
IKAIKGERHGKTVRVLDVAVKVRKKFLGREVEVWKLIFEHPQDVPAIRGKI
REHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETFYHEGD
EFGKGEIIMISYADEEEARVITWKNIDL PYVDVVSNEREMIKRFVQVVKE
KDPDVIITYNGDNFDLPYLIKRAEKLGVRLVLRDkehpEPKIQRMGDSF
AVEIKGRIFHDLFPVVRRTINLPTYTLEAVYEAIVLGTGKSKLGABEIAAI
WETEESMKKLAQYSMEDARATYELGKEFFPMEAELAKLIGQSVWDVSRSS
TGNLVEWYLLRVAYARNELAPNKPDEEYKRRLRTTYLGGYVKEPEKGLW
ENIYLDLFRSLYPSIIIVTHNVSPDTLEKEGCKNYDVAPIVGYRCKDFPG
FIPSLGDLIAMRQDIKKMKSTIDPIEKMLDYRQRAIKLLANSYGYM
GYPKARWYSKEACESVTAWGRHYIEMTIREIEEKFGFKVLYADTDGFYAT

IPGEKPELIKKAKEFLNYINSKLPGLLELEYEGFYLRGFFVTKKRYAVI
 DEEGRIITRGLVVRDWEIAKETQAKVLEAILKEGSVEKAVEVVRDVV
 EKIAYRVPLEKLVIEHQITRDLKDYKAIGHVAIAKRLAARGIKVKPGT
 IISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYIENQVLPVLRILEA
 FGyrKEDLRYQSSKQTGLDAWLK_r——

>Deep

MILDADYITEDGKPIIRIFKKENGFEKVEYDRNFRPYIYALLKDDSQIDE
 VRKITAERHKGIVRIIDAOKVRKKFLGRPIEVWRLYFEHPQDVPAIRDKI
 REHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGE
 EFAKGPIMISYADEEEAKVITWKKIDLPYVEVVSSEMIKRFKLVIRE
 KDPDVIITYNGDSFDLPYLKRAEKLGIKPLGRDGS—EPKMQRLGDMT
 AVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKKQVYAEIAEA
 WETGKGLERVAKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSS
 TGNLVEWYLLRKAYERNELAPNKPDEREYERRLRRESYAGGYVKEPEKGLW
 EGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFKCKDFPG
 FIPSLKRLLLDERQEIKRKMASKDPIEKKMLDYRQRAIKILANSYGYGY
 GYAKARWYCKEACSVTAWGREYIEFVRKELEEKFGFKVLYIDTDGLYAT
 IPGAKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKRYALI
 DEEGKIITRGLVVRDWEIAKETQAKVLEAILKHGNEEAVKIVKEVT
 EKLSKYEIPPEKLVIEHQITRPLHEYKAIGHVAVAKRLAARGVKVRPGM
 VIGYIVLRGDGPIKRAILAEFDLRKHKYDAEYIENQVLPVLRILEA
 FGyrKEDLRWQKTKQTGLTAWLNKK_k——

>JDF-3

MILDVDYITENCKPVIRVFKKENGFRIEYDREFEPYFYALLRDDSAIEE
 IKKITAERHGRVVKVRAEKVKKFLGRSVEVWVLYFTHPQDVPAIRDKI
 RKHPAVIDIYEYDIPFAKRYLIDKGLIPMEGEEELKLSFDIETLYHEGE
 EFGTGPILMISYADESEARVITWKKIDLPYVEVVSSEMIKRFKRVVKE
 KDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGRDGS—EPKIQRMGDRF
 AVEVKGRVHFDLYPVIRRTINLPTYTLEAVYEAIFGKPKKQVYAEIATA
 WETGEGLERVARYSMEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSS
 TGNLVEWFLLRKAYERNELAPNKPDERELARR—RggYAGGYVKEPERGLW
 DNIYVLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFKCKDFPG
 FIPSLGNNLEERQIKRKMATLDPLEKNLLDYRQRAIKILANSYGYGY
 GYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHAT
 IPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKRYAVI
 DEECKIITRGLVVRDWEIAKETQARVLEAILRHGDVEEAVRIVREVT
 EKLSKYEVPPEKLVIEHQITRELKDYKATGPHVAIAKRLAARGVKIRPGT
 VISYIVLKGSGRIGDRAIPFDEFDPTKHKYDADYIENQVLPVERILRA
 FGyrKEDLRYQKTRQVGLGAWLKPKGkkk

Sequence tree:

Tree constructed using UPGMA

((Pfu :0.000998,
 Deep :0.000998):0.000080,
 (Tgo :0.000905,
 KOD :0.000905):0.000032,
 JDF-3 :0.000937):0.000141):0.000067,
 Vent :0.001144);

Please note that only upper-case letters are considered to be aligned.

Alignment (DIALIGN format):

Pfu	1	MILDVDYITE	EGKPVIRLFK	KENGKFKIEH	DRTFRPYIYA	LLRDDSKIEE
Tgo	1	MILDTDYITE	DGKPVIRIFK	KENGFEKIDY	DRNFEPYIYA	LLKDDSAIED
KOD	1	MILDTDYITE	DGKPVIRIFK	KENGFEKIEY	DRTFEPYFYA	LLKDDSAIEE
Vent	1	MILDTDYITK	DGKPIIRIFK	KENGFEKIEL	DPHFQPYIYA	LLKDDSAIEE
Deep	1	MILDADYITE	DGKPIIRIFK	KENGFEKVEY	DRNFEPYIYA	LLKDDSQIDE
JDF-3	1	MILDVDYITE	NGKPVIRVFK	KENGFEFRIEY	DREFEPYFYA	LLRDDSAIEE

Pfu	51	VKKITGERHG	KIVRIVDVEK	VEKKFLGKPI	TVWKLYLEHP	QDVPTIREKV
Tgo	51	VKKITAERHG	TTVRVVRAEK	VKKKFLGRPI	EVWKLYFTHP	QDVPAIRDKI
KOD	51	VKKITAERHG	TVVTVKRVEK	VQKKFLGRPV	EVWKLYFTHP	QDVPAIRDKI
Vent	51	IKAIKGERHG	KTVRVLDVAVK	VRKKFLGREV	EVWKLIFEHP	QDVPAMRGKI
Deep	51	VRKITAERHG	KIVRIIDAOK	VRKKFLGRPI	EVWRLYFEHP	QDVPAIRDKI
JDF-3	51	IKKITAERHG	RVVKVKRAEK	VKKKFLGRSV	EVWVLYFTHP	QDVPAIRDKI

Pfu	101	REHPAVVDIF	EYDIPFAKRY	LIDKGLIPME	GEEELKILAF	DIETLYHEGE
Tgo	101	KEHPAVVDIY	EYDIPFAKRY	LIDKGLIPME	GDEELKMLAF	DIETLYHEGE
KOD	101	REHGAVIDIY	EYDIPFAKRY	LIDKGLVPM	GDEELKMLAF	DIQTLYHEGE
Vent	101	REHPAVVDIY	EYDIPFAKRY	LIDKGLIPME	GDEELKLLAF	DIETFYHEGD
Deep	101	REHSAVIDIF	EYDIPFAKRY	LIDKGLIPME	GDEELKLLAF	DIETLYHEGE
JDF-3	101	RKHPAVIDIY	EYDIPFAKRY	LIDKGLIPME	GEEELKLSMF	DIETLYHEGE

Pfu	151	EFGKGPIIMI	SYADENEAKV	ITWKNIDLPI	VEVSSSEREM	IKRFLRIIRE
Tgo	151	EFAEGPILMI	SYADEEGARV	ITWKNIDLPI	VDVSTEEKEM	IKRFLKVVE
KOD	151	EFAEGPILMI	SYADEEGARV	ITWKNVDLPY	VDVSTEREM	IKRFLRVVKE
Vent	151	EFGKGEIIMI	SYADEEEARV	ITWKNIDLPI	VDVSNEREM	IKRFVQVVE
Deep	151	EFAKGPIIMI	SYADEEEAKV	ITWKKIDLPI	VEVSSSEREM	IKRFLKVIRE
JDF-3	151	EFGTGPILMI	SYADESEARV	ITWKKIDLPI	VEVSTEEKEM	IKRFLRVVKE

Pfu	201	KDPDIIVTYN	GDSFDFPYLA	KRAEKLGIKL	TIGRDGS—E	PKMQRIGDMT
Tgo	201	KDPDVLITYN	GNFDFAYLK	KRSEKLGVKF	ILGREGS—E	PKIQRMGDRF
KOD	201	KDPDVLITYN	GNFDFAYLK	KRCEKLGINF	ALGRDGS—E	PKIQRMGDRF
Vent	201	KDPDVIITYN	GNFDFLPYLI	KRAEKLGVRL	VLGRDkehpe	PKIQRMGDSF
Deep	201	KDPDVIITYN	GDSFDFLPYLV	KRAEKLGIKL	PLGRDGS—E	PKMQRLGDMT
JDF-3	201	KDPDVLITYN	GNFDFAYLK	KRCEKLGVSF	TLGRDGS—E	PKIQRMGDRF

Pfu	249	AVEVKGRIHF	DLYHVITRTI	NLPTYTLEAV	YEAIFGPKPE	KVYADEIAKA
Tgo	249	AVEVKGRIHF	DLYPVIRRTI	NLPTYTLEAV	YEAIFGQPKPE	KVYAEIEIAQA
KOD	249	AVEVKGRIHF	DLYPVIRRTI	NLPTYTLEAV	YEAIFGQPKPE	KVYAEIEITPA



Vent	251	AVEIKGRIHF	DLFPVVRTI	NLPTYTLEAV	YEAVLGKTKS	KLGAEEIAAI
Deep	249	AVEIKGRIHF	DLYHVIRRTI	NLPTYTLEAV	YEAIFGPKPE	KVYAHEIAEA
JDF-3	249	AVEVKGRVHF	DLYPVIRRTI	NLPTYTLEAV	YEAVFGPKPE	KVYAEEIATA

Pfu	299	WESGENLERV	AKYSMEDAKA	TYELGKEFLP	MEIQLSRLVG	QPLWDVSRSS
Tgo	299	WETGEGLERV	ARYSMEDAKV	TYELGKEFFP	MEAQLSRLVG	QSLWDVSRSS
KOD	299	WETGENLERV	ARYSMEDAKV	TYELGKEFLP	MEAQLSRLIG	QSLWDVSRSS
Vent	301	WETEESMKKL	AQYSMEDARA	TYELGKEFFP	MEAEALAKLIG	QSVWDVSRSS
Deep	299	WETGKGLERV	AKYSMEDAKV	TYELGREFFP	MEAQLSRLVG	QPLWDVSRSS
JDF-3	299	WETGEGLERV	ARYSMEDARV	TYELGREFFP	MEAQLSRLIG	QGLWDVSRSS

Pfu	349	TGNLVEWFLL	RKAYERNEVA	PNKPSEEEYQ	RRLRESYTG	FVKEPEKGLW
Tgo	349	TGNLVEWFLL	RKAYERNELA	PNKPDERELA	RR-RESYAGG	YVKEPERGLW
KOD	349	TGNLVEWFLL	RKAYERNELA	PNKPDEKELA	RR-RQSYEGG	YVKEPERGLW
Vent	351	TGNLVEWYLL	RVAYARNELA	PNKPDEEEYK	RRLRTTYLGG	YVKEPEKGLW
Deep	349	TGNLVEWYLL	RKAYERNELA	PNKPDEREYE	RRLRESYAGG	YVKEPEKGLW
JDF-3	349	TGNLVEWFLL	RKAYERNELA	PNKPDERELA	RR-RggYAGG	YVKEPERGLW

DXSLYPSII (Region II)

Pfu	399	ENIVYLD FRA	LYPSIIITHN	VSPDTLNLEG	CKNYDIAPQV	GHKFCKDIPG
Tgo	398	ENIVYLD FRS	LYPSIIITHN	VSPDTLNREG	CEEYDVAPQV	GHKFCKDFPG
KOD	398	ENIVYLD FRS	LYPSIIITHN	VSPDTLNREG	CKEYDVAPQV	GHRFCKDFPG
Vent	401	ENIIYLD FRS	LYPSIIITHN	VSPDTLEKEG	CKNYDVAPIV	GYRFCKDFPG
Deep	399	EGLVSLD FRS	LYPSIIITHN	VSPDTLNREG	CREYDVAPV	GHKFCKDFPG
JDF-3	398	DNIVYLD FRS	LYPSIIITHN	VSPDTLNREG	CRSYDVAPV	GHKFCKDFPG

Pfu	449	FIPSLLG HLL	EERQIKTKM	KETQDPIEKI	LLDYRQKAIK	LLANSFYGY
Tgo	448	FIPSLLG DLL	EERQKVKKM	KATIDPIEKK	LLDYRQRAIK	ILANSFYGY
KOD	448	FIPSLLG DLL	EERQIKKKM	KATIDPIERK	LLDYRQRAIK	ILANSYGY
Vent	451	FIPSLG DLI	AMRQDIKKM	KSTIDPIEKK	MLDYRQRAIK	LLANSYGYM
Deep	449	FIPSLK RLL	DERQEIKRKM	KASKDPIEKK	MLDYRQRAIK	ILANSYGY
JDF-3	448	FIPSLG NLL	EERQIKRKM	KATLDPLEKN	LLDYRQRAIK	ILANSYGY

Pfu	499	GYAKARWYCK	ECAESVTAWG	RKYIELVWKE	LEEKFGFKVL	YIDTDGLYAT
Tgo	498	GYAKARWYCK	ECAESVTAWG	RQYIETTIRE	IEEKFGFKVL	YADTDGFFAT
KOD	498	GYARARWYCK	ECAESVTAWG	REYITMTIKE	IEEKYGFVKI	YSDTDGFFAT
Vent	501	GYPKARWYSK	ECAESVTAWG	RHYIEMTIRE	IEEKFGFKVL	YADTDGFYAT
Deep	499	GYAKARWYCK	ECAESVTAWG	REYIEFVRKE	LEEKFGFKVL	YIDTDGLYAT
JDF-3	498	GYARARWYCR	ECAESVTAWG	REYIEMVIRE	LEEKFGFKVL	YADTDGLHAT

Pfu	549	IPGGESEEEK	KKALEFVKYI	NSKLPGLLEL	EYEGFYKRGF	FVTKKRYAVI
Tgo	548	IPGADAETVK	KKAKEFLDYI	NAKLPGLLEL	EYEGFYKRGF	FVTKKKYAVI

KOD	548	IPGADAETVK	KKAMEFLNYI	NAKLPGALEL	EYEGFYKRGF	FVTKKKYAVI
Vent	551	IPGEKPELIK	KKAKEFLNYI	NSKLPGLLEL	EYEGFYLRGF	FVTKKRYAVI
Deep	549	IPGAKPEEIK	KKALEFVDYI	NAKLPGLLEL	EYEGFYVRGF	FVTKKKYALI
JDF-3	548	IPGADAETVK	KKAMEFLNYI	NPKLPGLLEL	EYEGFYVRGF	FVTKKKYAVI

Pfu	599	DEEGKVITRG	LEIVRRDWSE	IAKETQARVL	ETILKHGDVE	EAVRIVKEVI
Tgo	598	DEEDKITTRG	LEIVRRDWSE	IAKETQARVL	EAILKHGDVE	EAVRIVKEVT
KOD	598	DEEGKITTRG	LEIVRRDWSE	IAKETQARVL	EALLKGDGVE	KAVRIVKEVT
Vent	601	DEEGRITTRG	LEVVRDWSE	IAKETQAKVL	EAILKEGSVE	KAVEVVRDVV
Deep	599	DEEGKIITRG	LEIVRRDWSE	IAKETQAKVL	EAILKHGNVE	EAVKIVKEVT
JDF-3	598	DEEGKITTRG	LEIVRRDWSE	IAKETQARVL	EAILRHGDVE	EAVRIVREVT

Pfu	649	QKLANYEIPP	EKLAIYEQIT	RPLHEYKAIG	PHVAVAKKLA	AKGVKIKPGM
Tgo	648	EKLSKYEVP	EKLVIYEQIT	RDLKDYKATG	PHVAVAKRLA	ARGIKIRPGT
KOD	648	EKLSKYEVP	EKLVIHEQIT	RDLKDYKATG	PHVAVAKRLA	ARGVKIRPGT
Vent	651	EKIAKYRVPL	EKLVIHEQIT	RDLKDYKAIG	PHVAIAKRLA	ARGIKVKPGT
Deep	649	EKLSKYEIPP	EKLVIYEQIT	RPLHEYKAIG	PHVAVAKRLA	ARGVKVRPGM
JDF-3	648	EKLSKYEVP	EKLVIHEQIT	RELKDYKATG	PHVAIAKRLA	ARGVKIRPGT

Pfu	699	VIGYIVLRGD	GPISNRAILA	EEYDPKKHKY	DAEYYIENQV	LPAVLRILEG
Tgo	698	VISYIVLKGS	GRIGDRAIPF	DEFDPAKHKY	DAEYYIENQV	LPAVERILRA
KOD	698	VISYIVLKGS	GRIGDRAIPF	DEFDPTKHKY	DAEYYIENQV	LPAVERILRA
Vent	701	IISYIVLKGS	GKISDRVILL	TEYDPRKHKY	DPDYIENQV	LPAVLRILEA
Deep	699	VIGYIVLRGD	GPISKRAILA	EEFDLRKHKY	DAEYYIENQV	LPAVLRILEA
JDF-3	698	VISYIVLKGS	GRIGDRAIPF	DEFDPTKHKY	DADYYIENQV	LPAVERILRA

Pfu	749	FGYRKEDLRY	QKTRQVGLTS	WLNKKs—
Tgo	748	FGYRKEDLRY	QKTRQVGLGA	WLKPKt—
KOD	748	FGYRKEDLRY	QKTRQVGLSA	WLKPKgt—
Vent	751	FGYRKEDLRY	QSSKQTGLDA	WLKr——
Deep	749	FGYRKEDLRW	QKTKQTGLTA	WLNKKk—
JDF-3	748	FGYRKEDLRY	QKTRQVGLGA	WLKPKGkkk

Alignment (FASTA format):

```

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EFGKGPIIMISYADENEAKVITWKNIDLPYEVVSSEREMIKRFLRIIRE
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FIPSLGHLLEERQKIKTKMKETQDPIEKILLDYRQAIKLLANSFYGY
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DEEGKVITRGLIVRRDWSEIAKETQARVLETILKHGDVEEAVRIVKEVI
QKLANYEIPPEKLATIEQITRPLHEYKAIGHVAVAKLAARGVKIKPGM
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FGYRKEDLRYQKTRQVGLTSWLNKKS—

>Tgo

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EFAEGPILMISYADEEGARVITWKNIDLPHYVDVSTEKEMIKRFLKVVE
KDPDVLITYNGDNDFAYLKKRSEKLGKVFILGREGS—EPKIQRMGDRF
AVEVKGRIFHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKVKYABEIAQA
WETGEGLERVARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRSS
TGNLVEWFLLRKAYERNELAPNKPDERELARR—RESYAGGYVKEPERGLW
ENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFKCDFPG
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GYAKARWYCKEACESVTAWGRQYIETTIREIEEKFGFKVLYADTDGFFAT
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DEEDKITTRGLEIVRRDWSEIAKETQARVLEAILKHGDVEEAVRIVKEVT
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>KOD

MILDTDYITEDGKPVIRIFKKENGFEKIEYDRTFEPYFYALLKDDSAIEE
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KDPDVLITYNGDNDFAYLKKRCEKLGINFALGRDGS—EPKIQRMGDRF
AVEVKGRIFHFDLYPVIRRTINLPTYTLEAVYEAIVFGQPKVKYABEITPA
WETGENLERVARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRSS
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ENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHKFKCDFPG
FIPSLGDLLEERQKIKKKMKATIDPIERKLLDYRQAIKILANSYGY
GYARARWYCKEACESVTAWGREYITMTIKEIEEKYGFVYISDTDGFFAT
IPGADAETVKKKAMEFLNYINAKLPGALELEYEGFYKRGFFVTKKRYAVI
DEEGKITTRGLEIVRRDWSEIAKETQARVLEALLKDGDEKAVRIVKEVT
EKLSKYEVPPPEKLVIEQITRDLKDYKATGPHVAVAKRLAARGVIRPGT
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FGYRKEDLRYQKTRQVGLSAWLKPKgt—

>Vent

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 EKIAYRVPLEKLVIEHQITRDLKDYKAIGPHVAIAKRLAARGIKVKPGT
 IISYIVLKGSGKISDRVILLTEYDPRKHKYDPDYIENQVLPAVLRILEA
 FGyrKEDLRyQSSKQTGLDAWLK_r——

>Deep

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 VRKITAERHGKIVRIIDAOKVRKKFLGRPIEVWRLYFHPQDVPAPARDKI
 REHSAVIDIFEYDIPFAKRYLIDKGLIPMEGDEELKLLAFDIETLYHEGE
 EFAKGPIMISYADEEEAKVITWKKIDLPYEVVSSEREMIKRFLKVIRE
 KDPDVIITYNGDSFDLPYLKRAEKLGIKPLGRDGS—EPKMQRGLDMT
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 EGLVSLDFRSLYPSIIITHNVSPDTLNREGCREYDVAPEVGHKFKCDFPG
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 EKLSKYEIPPEKLVIEHQITRPLHEYKAIGPHVAVAKRLAARGVKVRPGM
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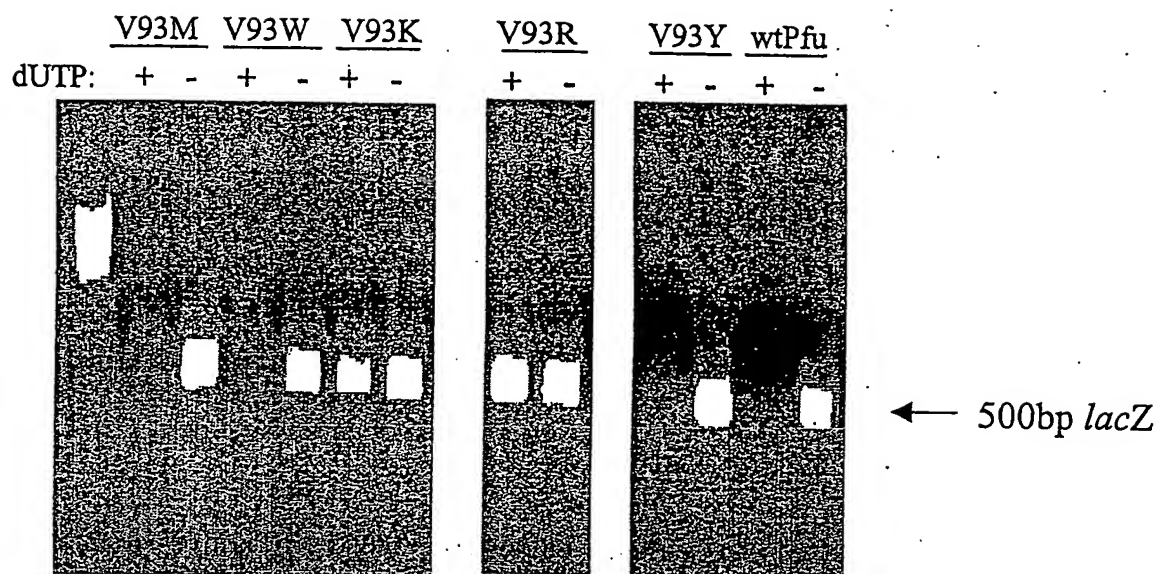
>JDF-3

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 KDPDVLITYNGDNFDFAYLKKRCEKLGVSFTLGRDGS—EPKIQRMGDRF
 AVEVKGVRVHFDLYPVIRRTINLPTYTLEAVYEAIFGKPKVKYAEHIAEA
 WETGGLERVARYSMEDARVTYELGREFFPMEAQLSRLIGQGLWDVSRSS
 TGNLVEWYLLRKAYERNELAPNKPDERELARR—R_{gg}YAGGYVKEPERGLW
 DNIYVYLDFRSLYPSIIITHNVSPDTLNREGCRSYDVAPEVGHKFKCDFPG
 FIPSLGNNLEERQIKRKMATLDPLEKNLLDYRQRAIKILANSYGYGY
 GYARARWYCRECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHAT
 IPGADAETVKKKAMEFLNYINPKLPGLLELEYEGFYVRGFFVTKKRYAVI
 DEEGKITTRGLEIVRRDWEIAKETQARVLEAILRHGDVEEAVRIVREVT
 EKLSKYEVPEKLVIEHQITRELKDYKATGPHVAIAKRLAARGVKIRPGT
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Sequence tree:

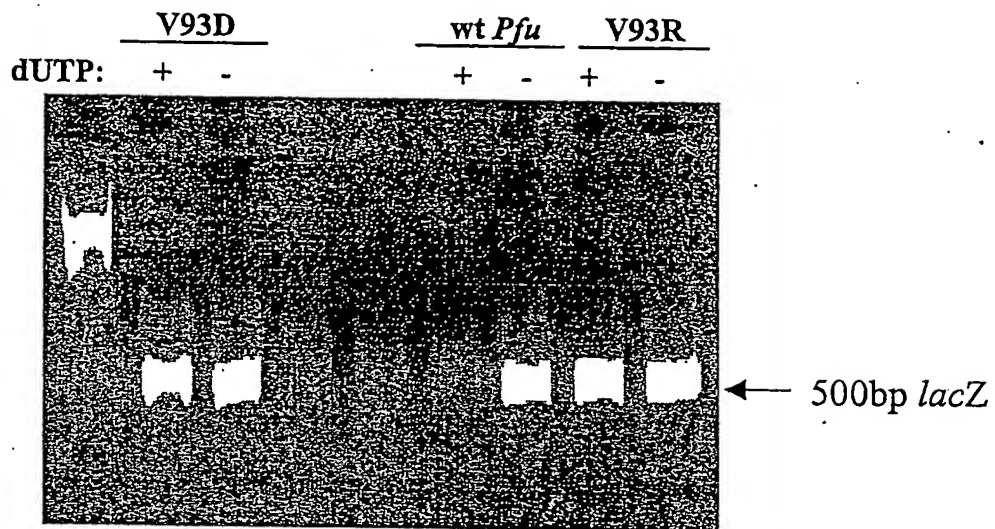
Tree constructed using UPGMA

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 ((Tgo :0.000905,
 KOD :0.000905):0.000032,
 JDF-3 :0.000937):0.000141):0.000067,
 Vent :0.001144);



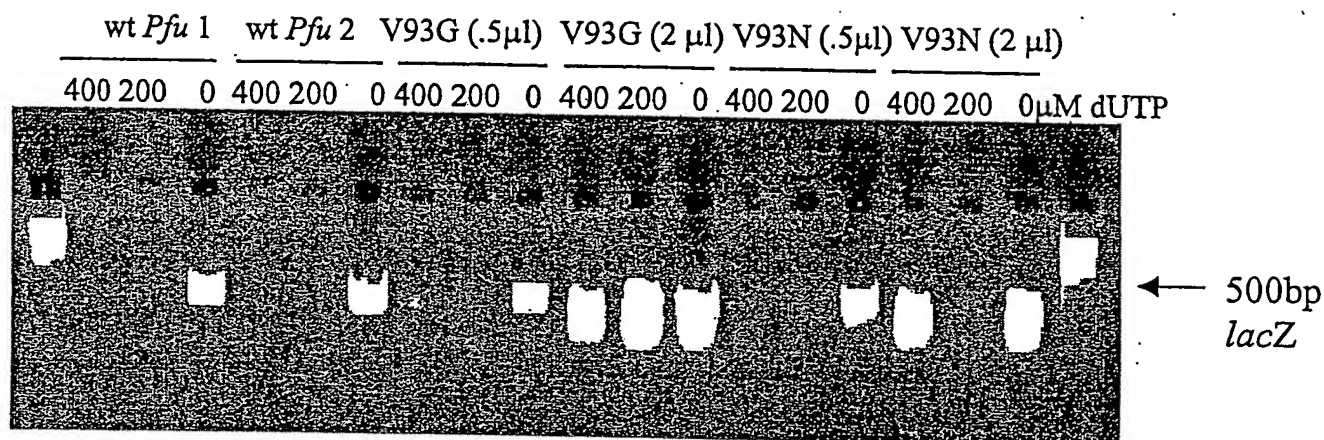
Results: *Pfu* V93K and V93R mutants show significantly improved dUTP incorporation compared to wild type *Pfu*. In contrast, the *Pfu* V93W, V93Y, and V93M mutants show little-to-no improvement in dUTP incorporation.

Figure 8A



Results: The *Pfu* V93D and V93R mutants show significantly improved dUTP incorporation compared to wild type *Pfu*.

Figure 8B



Results: The *Pfu* V93N mutant shows a very small improvement in dUTP incorporation compared to wild type *Pfu*. In contrast, the *Pfu* V93G mutant shows little-to-no improvement.

Figure 8C

Figure 9: Polymerase activity and Temperature optimum of Pfu N terminal truncation mutants

Pfu clone #	Truncated after Pfu residue	Relative DNA polymerase activity	Temperature Optimum
61	H30	Moderate	65°
72	V66	Similar to wild type	70°
81	P128	Low	Not tested
92	I158	Low	Not tested
3	G125	Similar to wild type	Not tested
13/14	K201	low	65°

Figure 10. Oligonucleotide Primers for QuikChange Mutagenesis

KOD V93 mutations

V93Q KOD 5' - CTCATCCG CAGGACCAGC CAGCGATAAG GGACAAG-3' (SEQ ID NO: 56)
V93R KOD 5' - CTCATCCG CAGGACCGTC CAGCGATAAG GGACAAG-3' (SEQ ID NO: 57)
V93K KOD 5' - CTCATCCG CAGGACAAAC CAGCGATAAG GGACAAG-3' (SEQ ID NO: 58)
V93N KOD 5' - CTCATCCG CAGGACAATC CAGCGATAAG GGACAAG-3' (SEQ ID NO: 59)
V93E KOD 5' - CTCATCCG CAGGACGAGC CAGCGATAAG GGACAAG-3' (SEQ ID NO: 60)
V93D KOD 5' - CTCATCCG CAGGACGATC CAGCGATAAG GGACAAG-3' (SEQ ID NO: 61)

Tgo V93 mutations

(SEQ ID NO: 62)

V93Q Tgo 5' -CAC CCC CAG GAC CAA CCC GCA ATC AGG GAC AAG G-3'

(SEQ ID NO: 63)

V93R Tgo 5' -CAC CCC CAG GAC AGA CCC GCA ATC AGG GAC AAG G-3'

(SEQ ID NO: 64)

V93N Tgo 5' -CAC CCC CAG GAC AAT CCC GCA ATC AGG GAC AAG G-3'

(SEQ ID NO: 65)

V93K Tgo 5' -CAC CCC CAG GAC AAA CCC GCA ATC AGG GAC AAG G-3'

(SEQ ID NO: 66)

V93E Tgo 5' -CAC CCC CAG GAC GAA CCC GCA ATC AGG GAC AAG G-3'

(SEQ ID NO: 67)

V93D Tgo 5' -CAC CCC CAG GAC GAC CCC GCA ATC AGG GAC AAG G-3'

JDF-3 V93 mutations

(SEQ ID NO: 68)

V93Q JDF-3 5'-ACG CAC CCG CAG GAC **CAG** CCG GCA ATC CGC GAC 3'

(SEQ ID NO: 69)

V93R JDF-3 5'-ACG CAC CCG CAG GAC **CGT** CCG GCA ATC CGC GAC 3'

(SEQ ID NO: 70)

V93E JDF-3 5'-ACG CAC CCG CAG GAC **GAG** CCG GCA ATC CGC GAC 3'

(SEQ ID NO: 71)

V93D JDF-3 5'-ACG CAC CCG CAG GAC **GAT** CCG GCA ATC CGC GAC 3'

(SEQ ID NO: 72)

V93K JDF-3 5'-ACG CAC CCG CAG GAC **ATA** CCG GCA ATC CGC GAC 3'

Pfu deletions

(SEQ ID NO: 73)

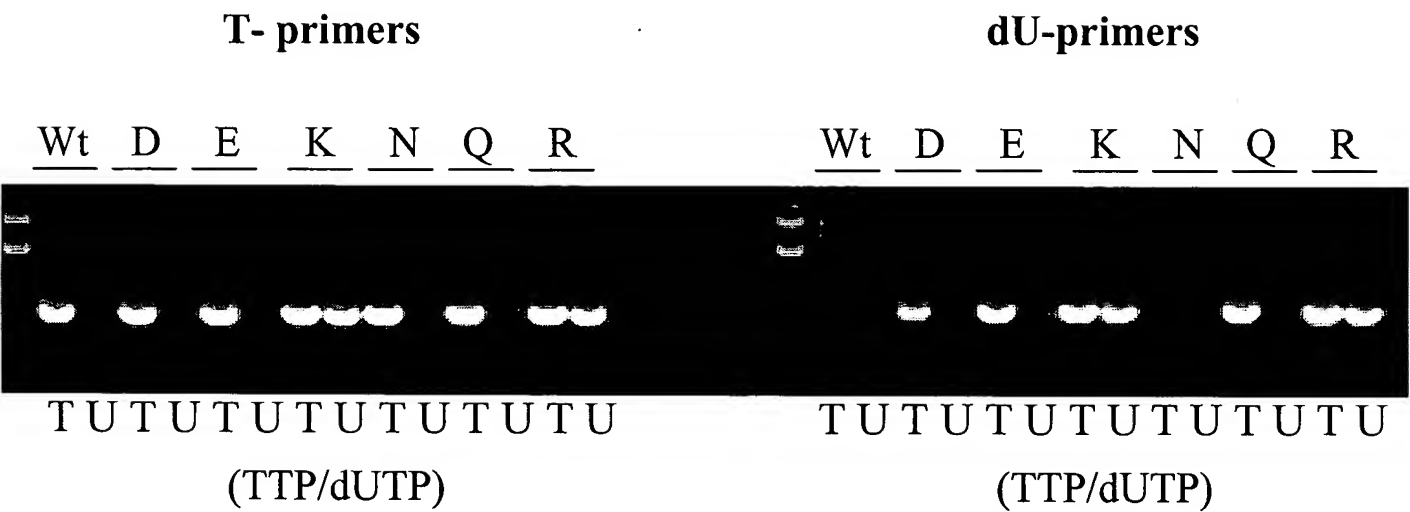
Δ93 Pfu : 5'- GAA CAT CCC CAA GAT CCC ACT ATT AGA G-3'

(SEQ ID NO: 74)

Δ92-94 Pfu : 5'- GAA CAT CCC CAA ACT ATT AGA G-3'

Fig. 11. Uracil Insensitivity of KOD V93 mutants

T-/dU-primers and dUTP/TTP incorporation:



	With regular primers		With U primers	
	dNTP	dGCAU	dNTP	dGCAU
KOD WT	+	-	-	-
KOD V93D	+	-	+	-
KOD V93E	+	-	+	-
KOD V93K	+	+	+	+
KOD V93N	+	-	-	-
KOD V93Q	+	-	+	-
KOD V93R	+	+	+	+

Fig. 12. Uracil Insensitivity of Tgo V93 mutants

T-primers and dUTP/TTP incorporation:

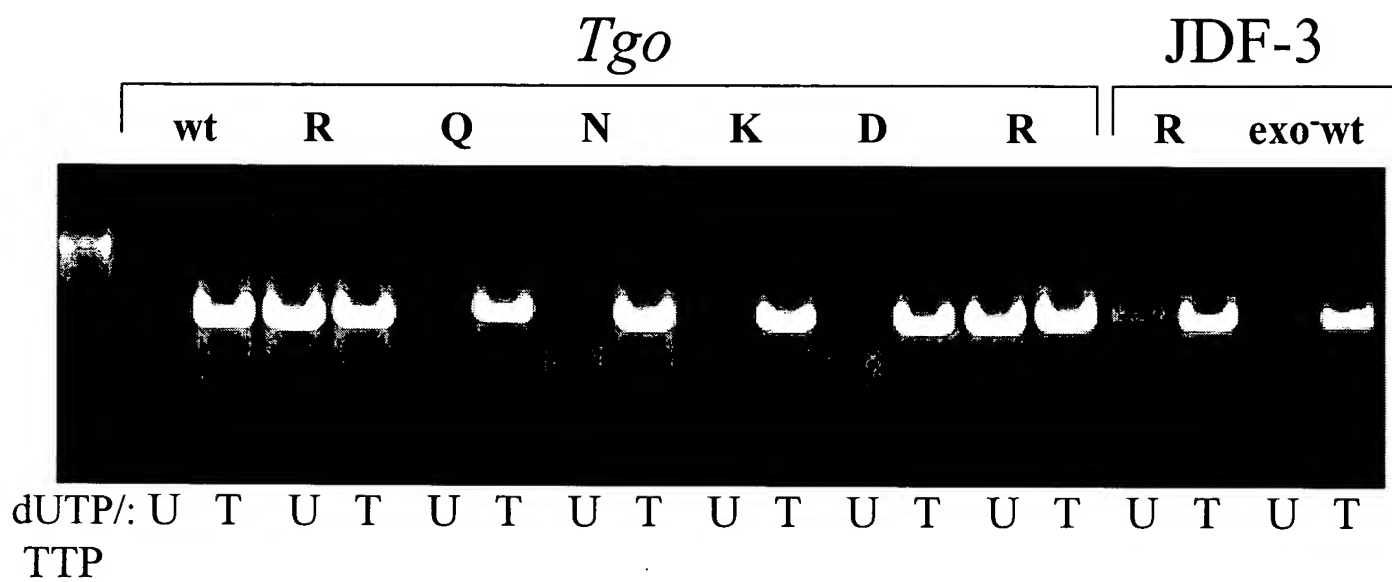
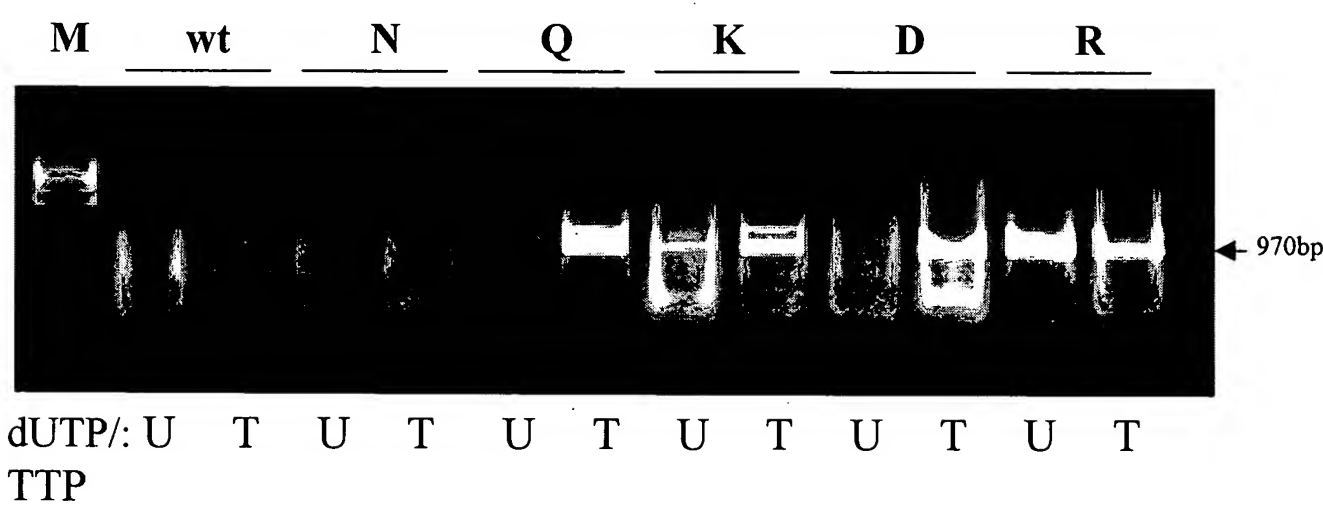


Fig. 13. Uracil Insensitivity of JDF-3 V93 mutants

T-primers and dUTP/TTP incorporation:



T-/dU-primers and dUTP/TTP incorporation:

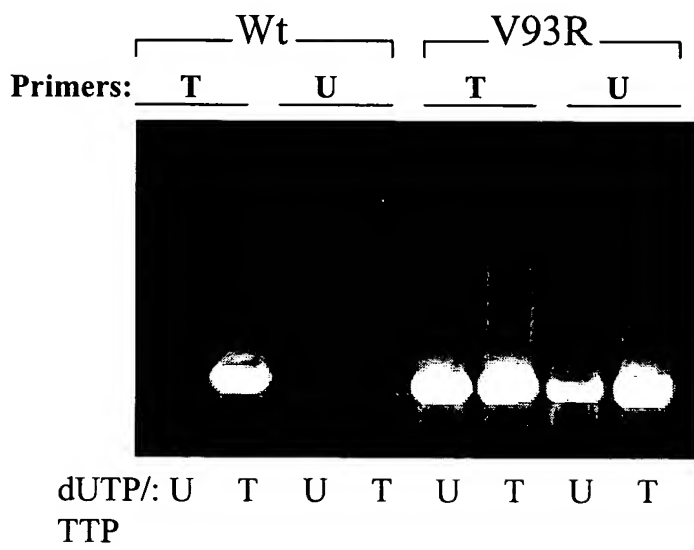
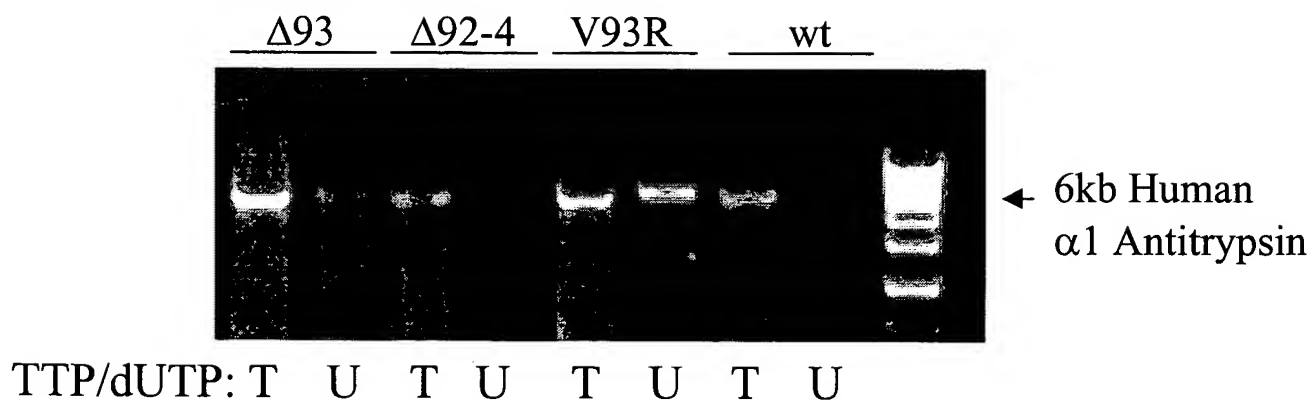
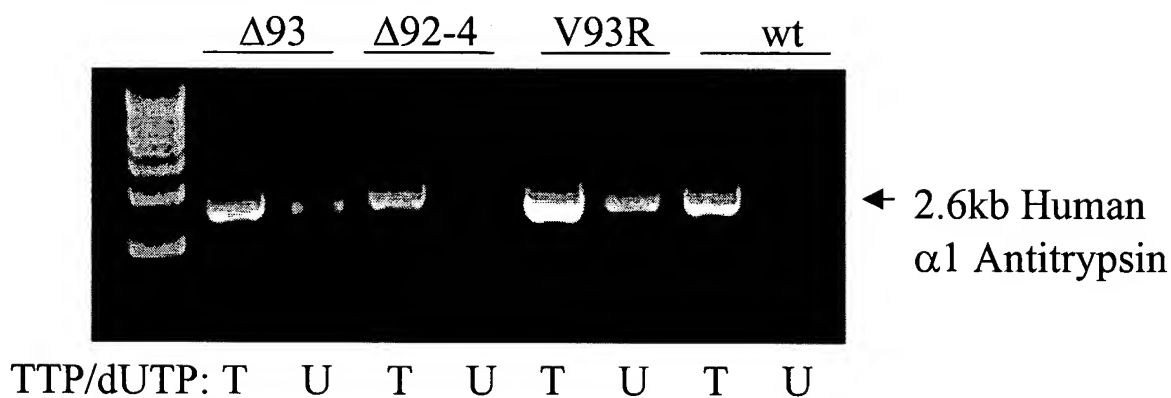
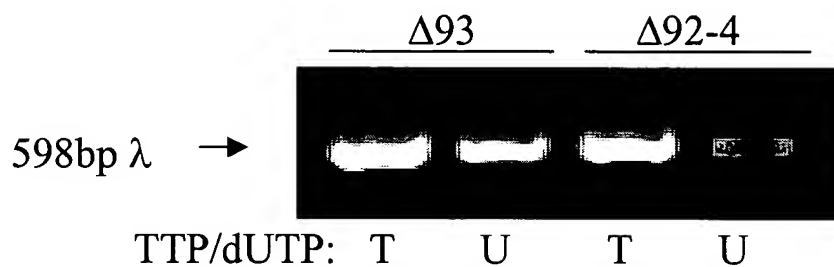
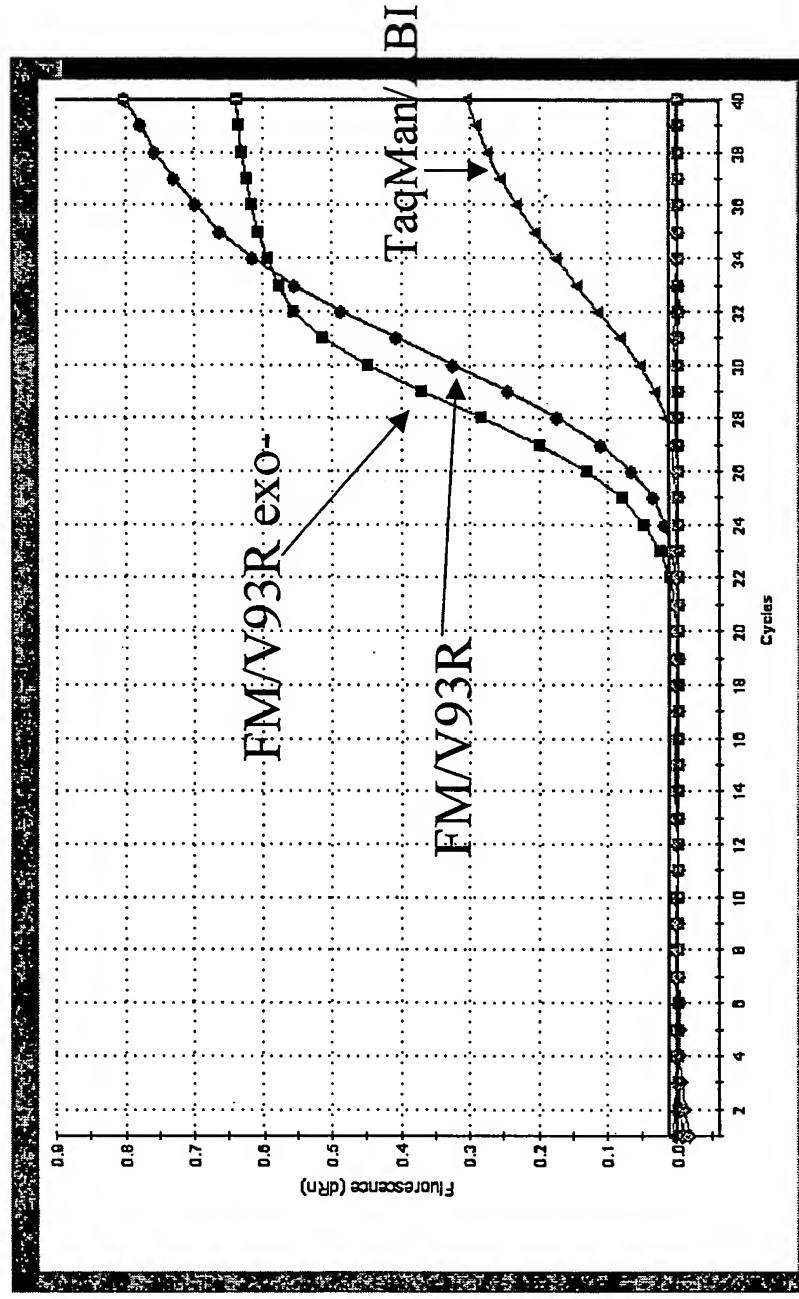


Fig. 14. Uracil Sensitivity of *Pfu* deletion mutants

T-primers and dUTP/TTP incorporation:



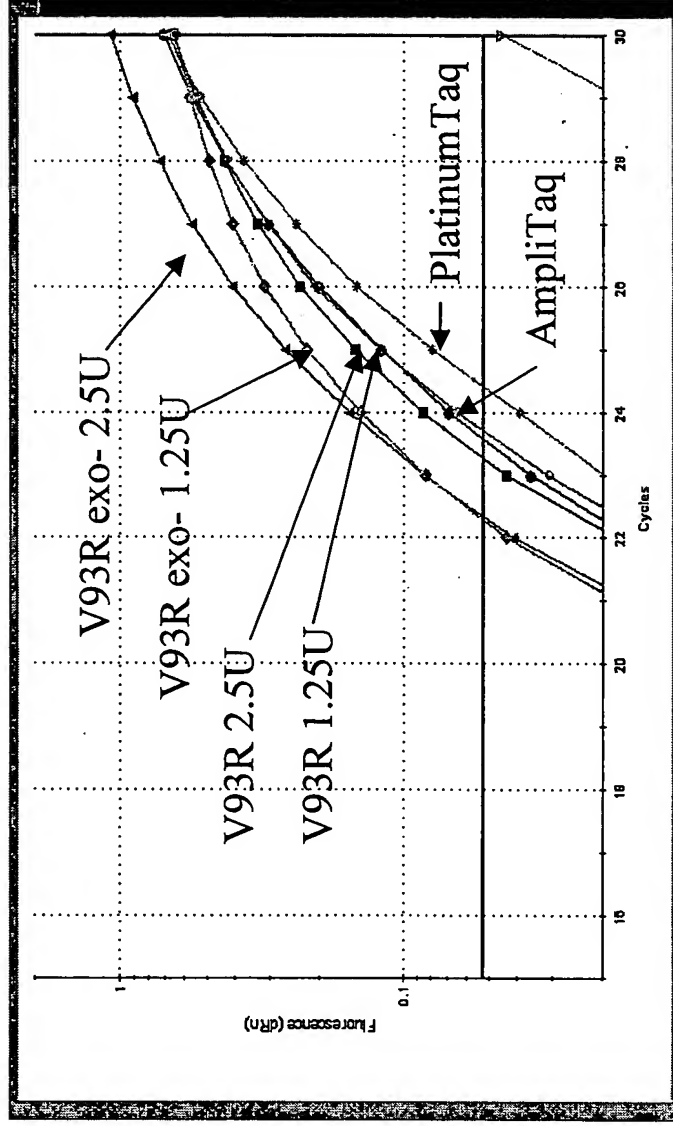
Amplification Plot for Comparison of Three Polymerases in QRT-PCR



* FM = FEN-1

Figure 15

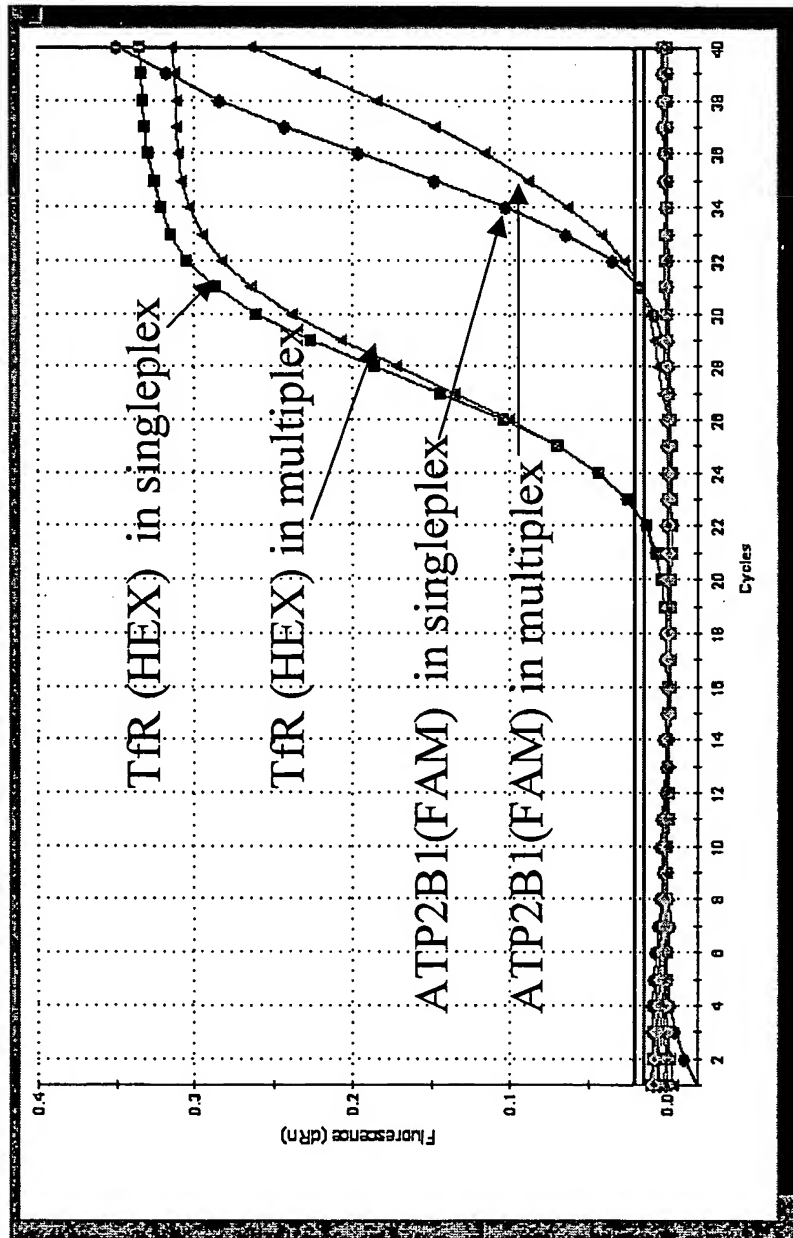
Semi-log Amplification Plots Comparing Pfu V93R and Pfu V93R exo- Containing QPCR Reactions



	V93R exo-	V93R exo-	V93R	V93R	PlatinumTaq	AmpliTaq
Units	1.25	2.5	1.25	2.5	1.25	1.25
Avg Ct	22.2	22.2	23.5	23.2	24.3	23.6

Figure 16

Pfn V93R exo -*Multiplex-ATP2B1 and Tfr*



	Target amt	Tfr	ATP2B1	Tfr + ATP2B1
Pfn V93R exo	100ng	22.8		22.7
			30.9	30.8
ABIMM	100ng	24.6		25.3
(TaqMan)			30.3	30.1

Figure 17